

Descriptions of barley genetic stocks for 2011

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In this volume of the Barley Genetics Newsletter, eighty eight new and revised Barley Genetic Stock (BGS) descriptions are published (Table 1). The current lists of new and revised BGS descriptions, including those in Table 1, are presented by BGS number order (Table 2) and by locus symbol in alphabetic order (Table 3) in another section of this issue. Information on the description location, recommended locus name, chromosomal location, previous gene symbols, and the primary genetic stock (GSHO number and/or NGB number) are included in these lists. The GSHO stocks are held in the USDA-ARS Barley Genetic Stocks collection at the National Small Grains Collection (U.S. Department of Agriculture – Agricultural Research Service, National Small Grains Germplasm Research Facility, 1691 S 2700 W) Aberdeen, ID 83210, USA. The NGB stocks are held in the Nordic Genetic Resource Center (Nordgen), P.O. Box 41, SE-230 53 Alnarp, Sweden. This information is available through the Internet at the following addresses:

- (1) www.ars.usda.gov/PacWest/Aberdeen
- (2) www.ars-grin.gov:7000/npgs/descriptors/barley-genetics (GRIN)
- (3) <http://wheat.pw.usda.gov/ggpages/bgn/>
- (4) <http://www.nordgen.org/sesto>
- (5) <http://ace.untamo.net>

Table 1. A listing of Barley Genetic Stock (BGS) descriptions published in volume 41 of the Barley Genetics Newsletter, giving recommended locus symbols and names, chromosomal locations, and stock source information.

BGS no.	Locus symbol*		Chr. loc. [†]	Locus name or phenotype	Descr. vol. p.	GSHO no. [‡]
	Rec.	Prev.				
1	brh1	br, ari-i	7HS	Brachytic 1	41:58	25
2	fch12	f _c , clo-fc	7HS	Chlorina seedling 12	41:60	36
5	fch8	f8, clo-f8	7HS	Chlorina seedling 8	41:62	40
9	dsp1	l	7HS	Dense spike 1	41:63	1232
10	lks2	lk2, lk4	7HL	Short awn 2	41:66	566
11	ubs4	u4, ari-d	7HL	Unbranched style	41:69	567
13	des4	des4	7H	Desynapsis 4	41:71	595
14	des5	des5	7HL	Desynapsis 5	41:73	596
24	fst3	fs3	7HS	Fragile stem 3	41:74	1746
28	ert-a	ert-a	7HS	Erectoides-a	41:76	468
42	Pyr1	Pyr.g, Pyr.i	3HL	Pyramidatum 1	41:78	1581
45	sdw4		7HL	Semidwarf 4	41:80	
61	trp1	tr	4HL	Triple awned lemma 1	41:82	210
75	Lks1	Lk	2HL	Awnless 1	41:84	44
78	mtt4	mtt,,e, mt	2HL	Mottled leaf 4	41:86	1231
79	wst7	rb	2HL	White streak 7	41:87	247
82	Zeo1	Ert-r, Knd	2HL	Zeocriton 1	41:89	1613
93	ert-zd	ert-zd, br7	7HL	Erectoides-zd	41:91	504
99	lin1	s, rin	2HS	Lesser internode number 1	41:92	2492
102	uzu1	uz, u	3HL	Uzu 1 or semi brachytic 1	41:94	1300
107	wst1	wst, wst3	3HL	White streak 1	41:97	159
111	dsp10	l _c	3HL	Dense spike 10	41:99	71
124	vrs4	v4, int-e	3HL	Six-rowed spike 4	41:101	775
126	sld1	dw1	3HL	Slender dwarf 1	41:103	2488
129	wst6	wst,,j	3HL	White streak 6	41:105	2500
132	ari-a	lk7, ari-a	3HS	Breviaristatum-a	41:106	1648
134	ert-c	ert-c	3HL	Erectoides-c	41:108	471
172	lk5	lk5, ari-c	4HL	Short awn 5	41:110	1297
182	flo-a	flo-a	6H	Extra floret-a	41:112	1741
201	fch7	f7, clo-f7	1HL	Chlorina seedling 7	41:113	4
208	fst2	fs2	1HL	Fragile stem 2	41:114	578
214	eam8	ea _k , mat-a	1HL	Early maturity 8	41:116	765
231	cur5	cu5	2HS	Curly 5	41:120	1710
244	dsp11	dsp.am, dsp.ao	1HL	Dense spike 11	41:121	1722
252	eam7	ea7, ec	6HS	Early maturity 7	41:123	579
263	cur3	cu3	6HL	Curly 3	41:125	1707
264	mtt5	mt,,f	6HL	Mottled leaf 5	41:126	2410
302	mtt2	mt2	5HL	Mottled leaf 2	41:127	1398
322	dsk1	dsk	5HL	Dusky 1	41:128	1714
325	crl1	crl, cl	6H	Curly lateral 1	41:129	1211
326	blf1	bb	2HL	Broad leaf 1	41:130	1393

Table 1. (continued)

BGS no.	Locus symbol*		Chr. loc. [†]	Locus name or phenotype	Descr. vol. p.	GSHO no. [‡]
	Rec.	Prev.				
328	ari-e	ari-e	5HL	Breviaristatum-e	41:131	1653
330	ert-g	ert-g, br3	1HL	Erectoides-g	41:133	479
332	Ert-r	Ert-r	2HL	Erectoides-r	41:135	492
337	blf2	nlh, nl.k, bb2	5HL	Broad leaf 2	41:137	1667
339	lys3	sex3	5HL	High lysine 3	41:138	1785
343	Lbf1	Lfb	5HL	Leafy Bract 1	41:140	1577
352	gsh2	gs2, cer-b	3HL	Glossy sheath 2	41:141	736
353	gsh3	gs3, cer-a	7HS	Glossy sheath 3	41:143	737
354	gsh4	gs4, cer-x	6HL	Glossy sheath 4	41:146	738
355	gsh5	gs5, cer-s	2HL	Glossy sheath 5	41:149	739
387	des8	des8	3H	Desynapsis 8	41:151	599
389	des10	des.,p	5HL	Desynapsis 10	41:152	601
399	cer-d	cer-d	5HL	Eceriferum-d	41:153	425
402	cer-g	cer-g	2HL	Eceriferum-g	41:155	428
403	cer-h	cer-h	4HS	Eceriferum-h	41:157	429
404	cer-i	cer-i	5HL	Eceriferum-i	41:158	430
405	cer-k	cer-k	4HL	Eceriferum-k	41:160	432
407	cer-m	cer-m	1HL/3HL	Eceriferum-m	41:161	434
410	cer-p	cer-p	7HL	Eceriferum-p	41:162	437
412	cer-t	cer-t	5HL	Eceriferum-t	41:164	441
415	cer-w	cer-w	5HL	Eceriferum-w	41:166	1519
427	cer-zi	cer-zi	1HL	Eceriferum-zi	41:168	456
438	cer-zu	cer-zu	1HS	Eceriferum-zu	41:170	1528
445	cer-yb	cer-yb	2HL	Eceriferum-yb	41:171	1535
446	cer-yc	cer-yc	6H / 7HS	Eceriferum-yc	41:172	1536
465	msg28	msg.,as	2HS	Male sterile genetic 28	41:173	2380
475	lax-c	lax-c	6HL	Laxatum-c	41:174	1777
518	sdw1	denso	3HL	Semidwarf 1	41:176	2513
521	mtt1	mt, mt3	1H	Mottled leaf 1	41:179	622
522	cer-yi	cer-yi	2H	Eceriferum-yi	41:180	1542
545	int-i	int-i	2HS	Intermedium-i	41:181	1769
551	ari-f	ari-f	7H	Breviaristatum-f	41:182	1654
554	ari-m	ari-m	7HS	Breviaristatum-m	41:184	1661
555	ari-n	ari-n	7H	Breviaristatum-n	41:185	1662
556	ari-o	ari-o	7HL	Breviaristatum-o	41:186	1663
559	ari-r	ari-r	5H	Breviaristatum-r	41:187	1666
567	ert-v	ert-57	6H	Erectoides-v	41:188	497
595	ant4	rub	4H	Anthocyanin-deficient 4	41:189	1642
604	ant22	ant22	2HL	Anthocyanin-free 22	41:191	1635
614	Zeo2	Mo1, Zeo3	2HL	Zeocriton 2	41:193	637
621	Cal-c	Cal-c	5HL	Calcaroides-c	41:195	1567
630	Ari-s	ari-265	5H/7H	Breviaristatum-s	41:197	
635	nec7	nec-45	1H/6H/7H	Necroticans 7	41:198	2420
673	cst1	cs	5HL	Corn stalk	41:199	

Table 1. (continued)

BGS no.	Locus Symbol*		Chr. loc. [†]	Locus name or phenotype	Descr. vol. p.	GSHO no. [‡]
	Rec	Prev				
678	ari-u	ari-245	2HS	Breviaristatum-u	41:200	
679	acr4	acr-3	2H/6HL	Accordion rachis 4	41:201	
680	ari-v	ari-137	5HS	Breviaristatum-v	41:202	

* Recommended locus symbols are based on utilization of a three letter code for barley genes as approved at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on 05 August 1996.

[†] Chromosome numbers and arm designations are based on a resolution passed at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on 05 August 1996. The Burnham and Hagberg (1956) designations of barley chromosomes were 1 2 3 4 5 6 and 7 while new designations based on the Triticeae system are 7H 2H 3H 4H 1H 6H and 5H, respectively.

[‡] The seed stock associated with each BGS number is held as a GSHO stock number in the Barley Genetics Stock Collection at the USDA-ARS National Grains Germplasm Research Facility, Aberdeen, Idaho, USA.

BGS 1, Brachytic 1, *brh1*

Stock number: BGS 1
Locus name: Brachytic 1
Locus symbol: *brh1*

Previous nomenclature and gene symbolization:

Brachytic = *br* (11, 13).
Breviaristatum-*i* = *ari-i* (6, 9).
Dwarf x = *dx1* (7).

Inheritance:

Monofactorial recessive (11, 13).
Located in chromosome 7HS (4); about 9.3 cM distal from the *fch12* (chlorina seedling 12) locus (13); 0.8 cM distal from RFLP marker BCD129 (10); about 5.0 cM from AFLP marker E4134-8 in subgroup 1 of the Proctor/Nudinka map (12); about 13.6 cM proximal from SSR marker HVM04 in 7H bin 02 (2); *brh1.a* is associated with SNP markers 2_1419 to 2_0245 (positions 0.00 to 13.19 cM) in 7H bin 01 of the Bowman backcross-derived line BW074 (3); *brh1.x* is associated with SNP markers 1_0949 to 1_1495 (positions 0.00 to 8.77 cM) in 7H bin 01 of the Bowman backcross-derived line BW079 (3); *brh1.t* is associated with SNP markers 1_1495 to 1_0025 (positions 8.77 to 26.00 cM) in 7H bins 01 to 02 of the Bowman backcross-derived line BW078 (3); an unnamed *brh1* mutant is associated with SNP markers 1_0851 to 2_0485 (positions 17.32 to 121.90 cM) in 7H bins 02 to 07 of the Bowman backcross-derived line BW872 (3), likely in 1H bin 01 near the border with 1H bin 02.

Description:

Plants have short leaves, culms, spikes, awns, and kernels. The seedling leaf is about 2/3 normal length. A similar reduction in the size of other organs is observed, but the awns were less than 1/2 normal length (7). The mutant phenotype was easy to classify at all stages of growth. The approximately 20% reduction in kernel weight was caused primarily by a reduction in kernel length, 7.8 vs. 9.6 mm. Grain yields of the Bowman backcross-derived lines for *brh1* mutants were about 2/3 normal and lodging was greatly reduced (2). Börner (1) reported that *ari-i.38* seedlings are sensitive to gibberellic acid. Powers (11) stated that the assigned gene symbol for this mutant is *br* and that L.J. Stadler selected this symbol.

Origin of mutant:

A spontaneous mutant in Himalaya (Clho 1312) (11, 13).

Mutational events:

brh1.a (GSHO 25) in Himalaya (13); *brh1.c* (GSHO 229) in Moravian (PI 539135) (14); *ari-i.38* (NGB 115888, GSHO 1657) in Bonus (PI 189763) (9, 15); *brh1.e* (GSHO 1690) in Aramir (PI 467786) (15); *brh1.f* (*dx1*, GSHO 1422) in Domen (Clho 9562) (7); *brh1.t* (OUM136, GSHO 1691) in Akashinriki (PI 467400, OUJ659); *brh1.x* (7125, GSHO 1692) in Volla (PI 280423); *brh1.z* (Hja80001) in Aapo; *brh1.aa* (Hja80051) in a Hja80001 cross (5, 8); *brh1.ae* (FN053) in Steptoe (Clho 15229) (5); an unnamed variant in L50-200 (Alb Acc 67A, GSHO 1217) (16).

Mutant used for description and seed stocks:

brh1.a in Himalaya (GSHO 25); *ari-i.38* (GSHO 1657, NGB 115888) in Bonus, *brh1.a* in Bowman (PI 483237)*7 (GSHO 1820, BW074, NGB 20491); *ari-i.38* in Bowman*6 (GSHO 1821, BW047, NGB 20455); *brh1.e* in Bowman*7 (GSHO 1822, BW077, NGB 20484); *brh1.t* in Bowman*7 (GSHO 1823, BW078, NGB 20485); *brh1.x* in Bowman*7 (GSHO 1824, BW079, NGB 20486); *brh1.z* in Bowman*7 (GSHO 2179, BW080, NGB

20487); *brh1.aa* in Bowman*6 (GSHO 1668, BW075, NGB 20482); *brh1.ae* in Bowman*4 (BW076, NGB 20483).

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BGS 2, Chlorina seedling 12, *fch12*

Stock number: BGS 2
Locus name: Chlorina seedling 12
Locus symbol: *fch12*

Previous nomenclature and gene symbolization:

Chlorina seedling-c = f_c (5).
Chlorina seedling-fc = *clo-fc* (9).

Inheritance:

Monofactorial recessive (5).
Located in chromosome 7HS (2, 6); about 3.6 cM distal from the *gsh3* (glossy sheath 3) locus (8); about 9.3 cM proximal from the *brh1* (brachytic 1) locus (10); in 7H bin 02 about 2.3 cM from RFLP marker KFP027 and co-segregating with markers BCD130 and ABC327 (7); *fch12.b* is associated with SNP markers 2_0242 to 2_0495 (positions 6.89 to 32.35 cM) in 7H bins 01 to 03 of the Bowman backcross-derived line BW354 (1). in 7H bin 02.

Description:

Seedling leaves are yellow with green tips and new leaves show a yellow base and a green tip. As the plant develops, leaf color changes to pale green (5). Plants are vigorous, but anthesis is delayed by 6 to 10 days. Kernel weights of BW354 vary from similar to those of Bowman to 10% less. Grain production of BW354 is 1/2 to 2/3 of that of Bowman (3).

Origin of mutant:

A spontaneous mutant in Colseess (Clho 2792) (5).

Mutational events:

fch12.b (f_c) in Colseess (Colseess V, (GSHO 36) (5); *fch12.l* (Trebi chlorina 453, GSHO 155), *fch12.m* (Trebi V, GSHO 158), *fch12.n* (Trebi IX, GSHO 18), *fch12.o* (Trebi XI, GSHO 163) in Trebi (PI 537442) (4); *clo-fc.110* in Bonus (PI 189763) (9); *fch12.b* may be present in the brachytic chlorina stocks (GSHO 124 and GSHO 174) (11).

Mutant used for description and seed stocks:

fch12.b in Colseess (GSHO 36); *fch12.b* in Bowman (PI 483237)*7 (GSHO 1826), in Bowman*8 (BW354, NGB 20593).

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BGS 5, Chlorina seedling 8, *fch8*

Stock number: BGS 5
Locus name: Chlorina seedling 8
Locus symbol: *fch8*

Previous nomenclature and gene symbolization:

Chlorina seedling 8 = *f8* (4).
Chlorina seedling-f8 = *clo-f8^{f8}* (6).

Inheritance:

Monofactorial recessive (4).
Located in chromosome 7HS (2, 4, 5); about 13.0 cM distal from the *nud1* (naked caryopsis 1) locus (2, 4); about 2.7 cM distal from the *msg10* (male sterile genetic 10) locus (2); *fch8.j* is associated with SNP markers 1_1014 to 2_0445 (positions 80.65 to 121.90 cM) in 7H bins 06 to 07 of the Bowman backcrossed-derived line BW105 (1), likely in 7H bin 06.

Description:

Seedlings have a yellow-green color and plants retain a chlorina (yellow green) phenotype until ripening (2). Plants of Bowman backcross-derived line BW105 were viable in the field, but heading was delayed 2 to 10 days across environments. Plant height of BW105 varied from slight taller than Bowman to 3/3 of Bowman height and awns were slightly shorter. Spikes of BW105 had 2 to 3 more kernels than those of Bowman, seed weights were approximately 10% lower. Grain yields were 1/2 to 3/4 of those of Bowman (3).

Origin of mutant:

A spontaneous mutant in Comfort (Clho 4578) (4).

Mutational events:

fch8.j in Comfort (Comfort No II, GSHO 40) (4).

Mutant used for description and seed stock:

fch8.j in Comfort (GSHO 40); *fch8.j* in Bowman (PI 483237)*8 (GSHO 1829, BW364, NGB 20603).

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BGS 9, Dense spike 1, *dsp1*

Stock number: BGS 9
Locus name: Dense spike 1
Locus symbol: *dsp1*

Previous nomenclature and gene symbolization:

Dense spike = *l* (19, 22).

Lax spike = *L*₁ (9).

Short spike = *e* (21).

Inheritance:

Monofactorial recessive (1, 6, 22).

Located in chromosome 7HS (7, 9); about 10.5 cM distal from the *nud1* (naked caryopsis 1) locus (18, 19); near molecular marker cMWG704 (11); located near the centromere (11, 20); near markers Bmag0359 and Bmag0321 (20); *dsp1.a* is associated with SNP markers 2_0671 to 2_0485 (positions 93.97 to 121.90 cM) in 7H bins 06 to 07 of the Bowman backcross-derived line BW375 (2); *dsp1.ap*, *dsp1.aq*, *dsp1.ar*, and *dsp1.at* have in common from their donor parent Volla SNP markers 1_0299 to 2_0485 (positions 101.23 to 121.90 cM) in 7H bin 07 of the Bowman backcross-derived lines BW263 to BW266 (2); *dsp1.ae*, *dsp1.ag*, *dsp1.ah*, and *dsp1.af* (formerly called *Pyr.af*) have Haisa-type of SNP marker patterns in the region from 1_0128 to 1_0169 (positions 97.66 to 142.55 cM) in 7H bins 07 to 08 of the Bowman backcross-derived lines BW255, BW256, BW257, and BW654 (2); *dsp1.aa* (formerly *pyr.aa*), *dsp1.ac*, *dsp1.ay*, and *dsp1.az* (BW652, BW254, BW271, and BW272, respectively) originated from different cultivars, but retained SNP marker in the centromeric region of 7H identical to those of the Haisa-type (2); *dsp1.f* (formerly *Zeo.f*) is associated with SNP markers 1_1098 to 1_0303 (positions 68.46 to 120.92 cM) in 7H bin 07 of the Bowman backcross-derived line BW935 (2); *dsp1.a* with *nud1.a* and *fst3.c* is associated with SNP markers 2_0671 to 2_0485 (positions 93.97 to 121.90 cM) in 7H bins 06 to 07 of the Bowman backcross-derived line BW375 (2), in 7H bin 07.

Description:

Spike length is reduced because rachis internode length is reduced to about 2/3 normal. The reduction in rachis internode length caused by the *dsp1.a* and *uzu1.a* (*uzu* 1) alleles is similar and additive (16, 19). In F₂ progenies, the *dsp1.a* gene has pleiotropic effects on coleoptile length, culm length, and grain size (16). The original mutant line for *dsp1.ah* (Mut. 4841) was associated with increased grain yield (12), but the Bowman backcross-derived line with *dsp1.ah* yielded less than half as much as Bowman (3). The rachis internode lengths of the Bowman backcross-derived lines from Volla mutants (BW263 to BW266) averaged 2.7 mm compared to 4.5 mm for Bowman. Plants were slightly shorter than Bowman, kernels were shorter 8.7 vs. 9.8 mm and slightly wider, and kernels weights were about 10% lower (5.2 vs. 5.7 mg). BW264, which contains only the 7H segment from Volla, appeared to have a lower reduction in plant height and kernel weights (3). The BW lines with the donor parents Haisa (BW255, BW654), Freya (BW256), and Saale (BW257) headed about two days later than Bowman and were about 20% shorter. Kernels were shorter and about 20% lighter. Awns of BW lines having Haisa-type as a donor were shorter, 9 vs. 11 cm, and grain yields were less than 50% of the Bowman yields. The Haisa line (BW654) retaining only a 7H region from the donor parent was later and shorter than the other Haisa-type lines (3). The BW lines with a Volla mutant differed from the BW lines with a Haisa mutant by only one SNP marker, 1_1219 at 107.44 cM (3). Phenotypically, BW254 with *dsp1.ac*, BW271 with *dsp1.ay*, and BW272 with *dsp1.az* were similar to the BW lines from Volla, while BW652 with

dsp1.aa was similar to the BW lines from Haisa. Since BW lines from Haisa and Volla having other phenotypic variants have the same SNP marker heterogeneities in 7H lack the dense spike trait, the mutants named in this BGS description are likely independent mutants at the *dsp1* locus (2, 3). BW935 with *dsp1.f* was morphological similar to the BW lines with the Haisa mutants. The internode lengths in BW375 with *dsp1.a* were similar to those of other presumed *dsp1* mutants, but other morphological traits were affected by the presence of the *fst3.c* gene (3).

Origin of mutant:

Natural occurrence in cultivars from China, Japan, and Korea (22); X-ray induced mutants in Donaria and Haisa (13, 14); induced mutants in Haisa II (5).

Mutational events:

dsp1.a in many cultivars of Oriental origin, often associated with the short awn gene (16); *dsp1.f* (formerly called *Zeo.f*) (18:15:4l, GSHO 2137) in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (8); *dsp1.aa* (formerly *pyr.aa*) (Betzes Erectoides, Clho 10871, GSHO 2431) in Betzes (PI 129430) (10); *dsp1.ac* (Mut. 2654, GSHO 1716) in Donaria (PI 161974) (13); *dsp1.ae* (Mut. 4014, GSHO 1717), *dsp1.af* (formerly *Pyr.af*) (Mut. 4158, GSHO 1718) in Haisa (PI 197617) (13), *dsp1.ag* (Mut. 4551, GSHO 1719) in Freya (PI 290197) (14), *dsp1.ah* (Mut. 4841) in Saale (Pirolina, PI 539132) (12); *dsp1.ap* (7112, GSHO 1724), *dsp1.aq* (7113, GSHO 1725), *dsp1.ar* (7114, GSHO 1726), *dsp1.at* (7117, GSHO 1727) in Volla (PI 280423) (4, 5); *dsp1.ay* (WA11005-81, GSHO 1729) in WA9037-75 (see PI 639908 for pedigree) (23); *dsp1.az* (Wa1628-85) in Hazen (PI 483238) (23).

Mutant used for description and seed stocks:

dsp1.a in Honen 6 (OUJ469, PI 307495, GSHO 1232); *dsp1.aa* (Betzes Erectoides, Clho 10871, GSHO 2431) in Betzes; *dsp1.ar* in Volla (GSHO 1726); *dsp1.f* in Bowman*7 (GSHO 2137, BW935, NGB 22364); *dsp1.aa* in Bowman*4 (GSHO 2236), in Bowman*6 (BW652, NGB 22217); *dsp1.ac* in Bowman*5 (GSHO 2237, BW254, NGB 22079); *dsp1.ae* in Bowman*4 (GSHO 2239), in Bowman*5 (BW255, NGB 22080); *dsp1.af* in Bowman*5 (GSHO 2142) in Bowman*6 (BW654, NGB 22219); *dsp1.ag* in Bowman*4 (GSHO 2240), in Bowman*5 (BW256, NGB 22081); *dsp1.ah* in Bowman*7 (BW257, NGB 22082); *dsp1.ap* in Bowman*4 GSHO 2245), in Bowman*5 (BW263, NGB 22088); *dsp1.aq* in Bowman*5 (GSHO 2246), in Bowman*6 (BW264, NGB 22089); *dsp1.ar* in Bowman*7 (GSHO 1942, BW265, NGB 22090); *dsp1.at* in Bowman*5 (GSHO 2247, BW267, NGB 22092); *dsp1.ay* in Bowman*3 (GSHO 2250, BW271, NGB 22096); *dsp1.az* in Bowman*5 (BW272, NGB 22097); *dsp1.a* with *nud1.a* and *fst3.c* from Kobinkatagi 4 (OUM 382, GSHO 1746) in Bowman*6 (GSHO 1842), in Bowman*7 (BW375, NGB 20614).

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BGS 10, Short awn 2, *lks2*

Stock number: BGS 10
Locus name: Short awn 2
Locus symbol: *lks2*

Previous nomenclature and gene symbolization:

Short awn = *a* (22, 23).
Short awn = *lk* (20).
Short awn 2 = *lk₁* (9).
Short awn 2 = *lk2* (14).
Short awn 4 = *lk4* (3, 7).

Inheritance:

Monofactorial recessive (8, 9, 17).
Located in chromosome 7HL (8, 19); estimates ranged from 7.9 to 10.5 cM distal from the *nud1* (naked caryopsis 1) locus (4, 17, 19); about 2.8 cM distal from molecular marker WG541 in 7H bin 05 (10); about 8.6 cM proximal from RFLP marker WG380B in 7H bin 08 (1); near EST-based marker k04151 and k06123 (21); *lks2.b* is associated with SNP markers 2_0790 to 2_0060 (positions 73.96 to 97.66 cM) in 7H bins 06 and 07 of the Bowman backcross-derived line BW492 (2), likely in 7H bin 07.

Description:

Awns of both central and lateral spikelets are reduced to about 3/5 of the long awned type. Texture of the short awn is finer and more flexible than that of the long awn, especially in non-uzu genotypes (19, 20). Kernel weights of *lks2* plants were slightly reduced and kernels per spike were slightly increased, but other traits remained unchanged (18). The Atlas near-isogenic lines for *lks2* (half awn) were found to respond better to environmental and genetic stress than the normal lines (15, 16). The awn length of heterozygotes in some crosses was shorter than that of the normal parent. Awns, as measured from the tip of the last fertile spikelet on the spike to the tip of the awn, of the Bowman backcross-derived line BW492 were about 1/2 as long as Bowman awns, 5 to 6 vs. 11 to 12 cm. Kernels of BW492 plants were slightly lighter than those of Bowman in some tests and kernel width was slightly less. Other agronomic traits were similar to those of Bowman (5).

Origin of mutant:

Spontaneous occurrence in some cultivars and distributed in China, Japan, Korea, and Nepal (7, 13, 17, 20).

Mutational events:

lks2.b in cultivars of Oriental origin, often associated with the *dsp1.a* (dense spike 1) gene (8, 16, 19); a possible mutant in Morex (CIho 15773) (12, 13).

Mutant used for description and seed stocks:

lks2.b in Honen 6 (OUJ469, PI 307495, GSHO 566) (20); *lks2.b* from Sermo (CIho 7776) in Betzes (PI 129430)*7 (CIho 16558, GP 36), *lks2.b* from Sermo in Compana (CIho 5438)*7 (CIho 16188, GP 40), *lks2.b* from Sermo in Decap (CIho 3351)*7 (CIho 16562, GP 44) (6); *lks2.b* from R.I. Wolfe's Multiple Recessive Stock (GSHO 3451) in Bowman (PI 483237)*9 (GSHO 1850, BW492, NGB 20720).

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BGS 11, Unbranched style 4, *ubs4*

Stock number: BGS 11
Locus name: Unbranched style 4
Locus symbol: *ubs4*

Previous nomenclature and gene symbolization:

Unbranched style 4 = *u4* (8).
Breviaristatum-15 = *ari-15* (4).
Breviaristatum-d = *ari-d* (2, 3, 4, 6).
Short awn 8 = *lk8* (9).

Inheritance:

Monofactorial recessive (6, 8).
Located in chromosome 7HL (6, 7, 8); about 8.0 cM distal from the *nud1* (naked caryopsis 1) locus (8); *ubs4.d* is associated with SNP markers 2_0103 to 1_0563 (positions 139.96 to 154.35 cM) in 7H bins 08 to 09 of the Bowman backcross-derived line BW884 (1); *ari-d.15* is associated with SNP marker 1_0169 (position 142.66 cM) in 7H bin 08 of the Bowman backcross-derived line BW041 (1); *ari-d.44* is associated with SNP markers 1_0056 to 2_0092 (positions 51.93 to 152.29 cM) in 7H bins 04 to 09 of the Bowman backcross-derived line BW035 (1), in 7H bin 08.

Description:

The stigma has only a few very short branches. This prevents normal pollen reception and reduces seed set to 13 to 30% in *uzu* type plants. Both the *uzu1.a* and *srh1.a* (short rachilla hair) genes interact with *ubs4.d* to further reduce in seed set. Pollen fertility is normal (8). Awn length is about 1/4 normal (4). Seed set on plants of the Bowman backcross-derived lines for *ari-d.15* and *ubs4.d*, BW041 and BW884, respectively, varied from about 10% for plants grown in greenhouses to nearly 50% for plants grown at Aberdeen, Idaho, USA (2). Awns of the Bowman backcross-derived-lines for *ubs4.d*, BW884, and *ari-d.15*, BW041, extended about 3 cm beyond the tip of the tip while those of Bowman extended about 11 cm (2). Grain yields of BW041 and BW884 ranged from 1/4 to 1/2 those of Bowman. Compared to Bowman, kernel weights varied from slightly less to slightly more. Other morphological traits were similar to those of Bowman (2).

Origin of mutant:

A spontaneous mutant in Ao Hadaka (OUJ159) (8).

Mutational events:

ubs4.d (GSHO 567) in Ao Hadaka (Ao Hadaka-hen) (8); *ari-d.15* (NGB 115861, GSHO 1652), *-d.35* (NGB 115884), *-d.51* (NGB 115901) in Bonus (PI 189763) (4); *ari-d.44* (NGB 115891), *-d.57* (NGB 115911) in Bonus (5); *ari-d.105* (NGB 115917), *-d.107* (NGB 115919), *-d.116* (NGB 115928), *-d.129* (NGB 115940), *-d.130* (NGB 115941), *-d.150* (NGB 115961), *-d.160* (NGB 115970), *-d.186* (NGB 115996), *-d.187* (NGB 115997), *-d.192* (NGB 116002), *-d.193* (NGB 116003), *-d.232* (NGB 116042), *-d.239* (NGB 116048), *-d.240* (NGB 116049), *-d.241* (NGB 116050), *-d.242* (NGB 116051), *-d.243* (NGB 116052), *-d.247* (NGB 116058) in Foma (CIho 11333), *-d.288* (NGB 116105) in Kristina (NGB 1500) (4).

Mutant used for description and seed stocks:

ubs4.d in Ao Hadaka (GSHO 567); *ari-d.15* in Bonus (GSHO 1652, NGB 115861); *ubs4.d* in Bowman (PI 483237)*6 (GSHO 1849), in Bowman*7 (BW884, NGB 22318); *ari-d.15* in Bowman*8 (GSHO 1848, BW041, NGB 20449); *ari-d.44* in Bowman*6 (BW035, NGB 20443).

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Revised:

J.D. Franckowiak and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:56.

J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:69-70.

BGS 13, Desynapsis 4, *des4*

Stock number: BGS 13
Locus name: Desynapsis 4
Locus symbol: *des4*

Previous nomenclature and gene symbolization:
None.

Inheritance:

Monofactorial recessive (5, 6).

Located in chromosome 7H (1); *des4.af* is associated with SNP markers 1_0772 to 2_0790 (positions 71.81 to 73.96 cM) in 7H bin 05 and markers 2_0311 to 2_1448 (positions 126.28 to 134.43 cM) in 7H bin 08 of Bowman backcross-derived line BW240 (1); *des4.d* is associated with SNP markers 1_838 to 2_1201 (positions 49.53 to 134.43 cM) in 7H bins 04 to 08 of Bowman backcross-derived line BW241 (1).

Description:

The chromosomes are paired during pachytene and undergo desynapsis during diplotene. The degree of desynapsis is $d = 3.3 \pm 2.2$ with a range from 7 ring bivalents ($d = 0$) to 3 rod bivalents plus 8 univalents ($d = 11$). Many of the univalents split longitudinally during anaphase I, and lagging chromosomes and micronuclei are observed frequently at telophase I. Microspore tetrads contained an average of 1.0 micronuclei per tetrad and the range was 0 to 10. Ovule fertility was about 18% (3). Plants of the Bowman backcross-derived line for *des4.af*, BW240, were similar to Bowman except grain yields were 25 to 50% lower. Kernels were about 10% lighter than those of Bowman in most trials (2).

Origin of mutant:

A spontaneous mutant in Betzes (PI 129430) (5, 6).

Mutational events:

des4.d (GSHO 595), *des4.h* in Betzes (5, 6); *des4.z*, *des4.aa*, *des4.ab*, *des4.ac*, *des4.ad*, *des4.ae*, *des4.af*, *des4.ag* in Klages (Clho 15487) (4, 7); all the Klages mutants may be identical because they were isolated from the same field (4).

Mutant used for description and seed stocks:

des4.d in Betzes (GSHO 595), *des4.d* in Bowman*5 (BW241, NGB 22068); *des4.af* in Bowman*7 (BW240, NGB 22067).

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Prepared:

J.M. Hernandez-Soriano, R.T. Ramage, and R.F. Eslick. 1973. *Barley Genet. Newsl.*

3:127.

Revised:

R.T. Ramage and J.F. Scheuring. 1976. Barley Genet. Newsl. 6:116.

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:58.

J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:71-72.

BGS 14, Desynapsis 5, *des5*

Stock number: BGS 14
Locus name: Desynapsis 5
Locus symbol: *des5*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (4, 5).
Located in chromosome 7HL (4); *des5.e* is associated with SNP markers 2_0139 to 2_1363 (positions 194.97 to 198.70 cM) in 7H bin12 and with SNP markers 1_1198 to 2_1275 (positions 73.70 to 104.73) of the Bowman backcross-derived line BW244 (1), most likely in 7H bin 12.

Description:
The chromosomes are paired during pachytene and undergo desynapsis during diplotene. The degree of desynapsis is 11.1 ± 2.6 ranging from 7 ring bivalents ($d = 0$) to 14 univalents ($d = 14$). Many univalents split longitudinally during anaphase I. Lagging chromosomes and micronuclei are observed frequently at telophase I. Microspore quartets contain an average of 4.5 micronuclei per quartet with a range of 0 to 18. Ovule fertility is about 7%. When crossed with non-allelic desynaptic lines, the F_1 's frequently show a low degree of desynapsis (up to 3 rod bivalents per cell) (3). Plants of the Bowman backcross-derived line for *des5.e*, BW244, exhibited variable seed set with grain yields from 1/4 to 1/2 those of Bowman. Plant heights of BW244 ranged from 90% of Bowman to the same height and kernels weights were 80% of those for Bowman to almost the same (2).

Origin of mutant:
A spontaneous mutant in Betzes (PI 129430) (4, 5).

Mutational events:
des5.e (GSHO 596), *des5.f*, *des5.g* in Betzes (4, 5).

Mutant used for description and seed stocks:
des5.e in Betzes (GSHO 596); *des5.e* in Bowman*4 (BW244, NGB 22070).

References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
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Prepared:
J.M. Hernandez-Soriano, R.T. Ramage, and R.F. Eslick. 1973. *Barley Genet. Newsl.* 3:128.

Revised:
J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:59.
J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:73.

BGS 24, Fragile stem 3, *fst3*

Stock number: BGS 24
Locus name: Fragile stem 3
Locus symbol: *fst3*

Previous nomenclature and gene symbolization:

Fragile stem 3 = *fs3* (5).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 7HS (1, 5), probably proximal from the *dsp1* (dense spike 1) locus based on linkage drag (4); *fst3.c* with *dsp1.a* and *nud1.a* is associated with SNP markers 2_0671 to 2_0485 (positions 93.97 to 121.90 cM) in 7H bins 06 to 07 of the Bowman backcross-derived line BW375 (1), in 7H bin 07.

Description:

The leaf and stem characteristics of *fst3* plants are similar to those of *fst1* plants. Leaves and stems are very fragile and easily broken when slightly bent (5). Plants are about 2/3 normal height when protected in the greenhouse, but in the field plants are weak and are easily damaged by wind. The dense spike 1 (*dsp1.a*) and the naked caryopsis 1 (*nud1.a*) genes are also present with the *fst3.c* gene in Bowman backcross-derived line BW375 (3). BW375 plants were about half the height of Bowman, heading was delayed 3 to 10 days, kernels weight were 30 to 40% lower, and grain yields were from 0 to 30% of those for Bowman (3). In the OUM382 mutant line, crystalline cellulose content was reduced by 25% to 50% compared with the OUJ066 wild-type line (1, 6, 7, 8), and these reductions were similar to those observed in the *fst2* mutant lines (1, 8). The number of cellulose synthesizing terminal complexes was reduced by 80% in the *fst3.c* mutant (6).

Origin of mutant:

A spontaneous mutant in Kobinkatagi 4 (OUJ066, PI 190757) (5).

Mutational events:

fst3.c in Kobinkatagi 4 (OUM382, GSHO 1746) (5).

Mutant used for description and seed stocks:

fst3.c in Kobinkatagi 4 (GSHO 1746, OUM382); *fst3.c* with *dsp1.a* and *nud1.a* in Bowman (PI 483237)*5 (GSHO 1842), in Bowman*7 (BW375, NGB 20614).

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Prepared:

T. Konishi and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:70.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:74-75.

BGS 28, Erectoides-a, *ert-a*

Stock number: BGS 28
Locus name: Erectoides-a
Locus symbol: *ert-a*

Previous nomenclature and gene symbolization:

Erectoides-6 = *ert-6* (3).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 7HS (4, 10, 11); about 11.4 cM distal from the *cer-f* (eceriferum-f) locus (8, 9, 12, 13, 14); about 11.7 cM distal from the *nud1* (naked caryopsis 1) locus (8, 9, 11); *ert-a.6* is associated with SNP markers 1_0394 to 2_0103 (positions 107.44 to 142.55 cM) in 7H bins 07 to 08 of the Bowman backcross-derived line BW303 (1), likely in 7H bin 07, but in the long arm.

Description:

Spikes of all alleles have a compact appearance caused by a reduction in rachis internode length, with rachis internode length values from 1.7 to 2.6 mm (11). The *ert-a.6* allele produces plants with shorter internodes than most other *ert-a* alleles. Plants with an allele at the *ert-a* locus are 10 to 15 cm shorter than parental cultivars (6). The effects of the *ert-a* mutant on spike density are partially reversed by GA₃ treatments (15, 16). Plants of the Bowman backcross-derived line with *ert-a.6*, BW303, headed slightly earlier than Bowman and were about 15% shorter. Rachis internode lengths were 2.7 vs. 4.5 mm and kernel lengths averaged 8.8 vs. 9.9 mm. The kernel weights for BW303 were about 10% less than those for Bowman and grain yields were up to 25% less than those of Bowman (2). Based on phenotypic traits SNP markers from Gull retained in BW303, *ert-a.6* may be allele at the dense spike 1 (*dsp1*) locus (2).

Origin of mutant:

An X-ray induced mutant in Gull (CIho 1145, GSHO 466) (5, 6).

Mutational events:

ert-a.6 (NGB 112609, GSHO 468), *-a.11* (NGB 112609) in Gull, *-a.13* (NGB 112614, GSHO 215) in Maja (PI 184884), *-a.19* (NGB 112621) *-a.21* (NGB 112622), *-a.21* (trans) (NGB 112623), *-a.23* (NGB 112624), *-a.28* (NGB 112628) in Bonus (PI 189763) (2, 3, 6), *-a.29* (NGB 112629) in Maja (6); *ert-a.36* (NGB 112637), *-a.38* (NGB 112638), *-a.49* (NGB 112648) in Bonus (4, 5); *ert-a.77* (NGB 112676) in Bonus (5); *ert-a.99* (NGB 112698) in Bonus (7); *ert-a.131* (NGB 112730), *-a.147* (NGB 112746), *-a.160h* (NGB 112759) in Bonus (11); *ert-a.160l* (NGB 112760), *-a.161* (NGB 112761) in Bonus (7); *ert-a.166* (NGB 112766) in Bonus, *-a.315* (NGB 112830), *-a.316* (NGB 112831) in Foma (CIho 11333) (11); *ert-a.323* (NGB 112838) in Foma (7); *ert-a.334* (NGB 112849), *-a.340b* (NGB 112856), *-a.341* (NGB 112857), *-a.343* (NGB 112859) in Foma (11); *ert-a.348* (NGB 112864) in Foma (7); *ert-a.350* (NGB 112866), *-a.364* (NGB 112880), *-a.368* (NGB 112834), *-a.378* (NGB 112894), *-a.388* (NGB 112903), *-a.406* (NGB 112922), *-a.433* (NGB 112949), *-a.481* (NGB 112997), *-a.494* (NGB 113010) in Foma (11); *ert-a.1180* (NGB 114058), *-a.1187* (NGB 114066), *-a.1193* (NGB 114072), *-a.1197* (NGB 114076), *-a.1203* (NGB 114082), *-a.1210* (NGB 114090), *-a.1219* (NGB 114099) in Bonus (7).

Mutant used for description and seed stocks:

ert-a.6 in Gull (GSHO 468, NGB 112609); *ert-a.6* in Bowman (PI 483237)*8 (GSHO 1844, BW303, NGB 20585).

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:74-75.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:76-77.

BGS 42, Pyramidatum 1, *Pyr1*

Stock number: BGS 42
Locus name: Pyramidatum 1
Locus symbol: *Pyr1*

Previous nomenclature and gene symbolization:

Pyramidatum g = *Pyr.g* (5).

Pyramidatum i = *pyr.i* (5).

Inheritance:

Monofactorial recessive (2), which enhances the effects of *Zeo2* (Zeocriton 2) (2, 3). Located in chromosome 3HL (2), *Pyr1.g* is associated with SNP markers 2_0410 to 1_0926 (positions 61.77 to 85.26 cM) in 3H bin 05 of the Bowman backcross-derived line BW660 and with a marker in 2HL bin 13 where *Zeo2* (Zeocriton 2) locus is located; *Pyr1.i* (previously *Pyr2.i*) is associated with SNP markers 1_0825 to 2_0704 (positions 61.77 to 100.48 cM) in 3H bins 05 to 06 of the Bowman backcross-derived line BW661 and with markers in 2HL bin 13 where *Zeo2* (Zeocriton 2) locus is located; *pyr1.aw* (previously *pyr.aw*) is associated with SNP markers 2_0890 to 2_0704 (positions 82.03 to 100.48 cM) in 3H bins 05 to 06 of the Bowman backcross-derived line BW662 (2), in 3H bin 05.

Description:

Hayes and Harlan (6) reported that one gene controlled spike density in the line Pyramidatum. Spike shape, parallel vs. truncate pyramidal, is considered of limited value as a key character, but it is used in description of barley cultivars (1). Spikes are about 2/3 of normal length and have rachis internode length values of about 2.5 mm. Plants homozygous for *Pyr1.g* have pyramid-shaped spikes because lower rachis internodes shorter than upper ones. Spikes of heterozygous plants are parallel or strap-shaped. Plants homozygous for *Pyr1.a* are slightly shorter and have stiffer straw (3). When combined with *Zeo2* (Zeocriton 2), spikes of *Pyr1* plants are about 2/3 of normal length and have rachis internode length values of about 2.3 mm. The plants have pyramid-shaped spikes because lower rachis internodes are shorter than upper ones. The Bowman backcross-derived lines BW660 and BW661 have this phenotype. BW662, also derived from Pokko, has a similar 3H segment retained, but rachis internodes are only slightly shorter than those of Bowman, 3.6 vs. 4.5 mm (3). Unlike BW660 and BW661, BW662 does not have SNP marker 2_0590 (position 218.47 cM in 2H bin 13) (2). The semi-compact spike trait of BW662 was associated with a recessive inheritance pattern in backcross-derived progenies. Culms and peduncles of plants in lines BW660 and BW661 were 10 to 20% shorter than Bowman while a height reduction was not observed in BW662 (3). Kernel shapes and weights and grain yields of the BW lines for *Pyr1* were similar to those of Bowman (3).

Origin of mutant:

Probably natural occurrence in Finnish cultivars (3), but isolated from a backcross of Pokko (PI 467770) to Hja80001 (GSHO 1689, DWS1246), which is a gamma-ray induced, brachytic mutant from Aapo (PI 467771) (7).

Mutational events:

Pyr1.g in Hja64202 (Pokko*3/Hja80001 mutant, DWS1242, GSHO 1581) (4, 7).

Mutant used for description and seed stocks:

Pyr1.g in Hja64202 (GSHO 1581); *Pyr1.g* in Bowman (PI 483237)*7 (GSHO 2149, BW660, NGB 22225); *Pyr1.i* from Pokko mutant Hja79010 (Pokko*3/Hja80001 mutant, GSHO 1582) (7) in Bowman*6 (GSHO 1941), in Bowman*7 (BW661, NGB 22226); *pyr1.aw* from Hja80089 (7) in Bowman*7 (GSHO 2040, BW662, NGB 22227).

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Prepared:

J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:82.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:78-79.

BGS 45, Semidwarf 4, *sdw4*

Stock number: BGS 45
Locus name: Semidwarf 4
Locus symbol: *sdw4*

Previous nomenclature and gene symbolization:

Culm length QTL on 7H = qCUL.ak-7H (4).

Inheritance:

Monofactorial recessive (3, 7).

Location in chromosome 7HL (4); about 1.2 cM from codominant STS marker ABG608 in bin 11 (3, 4); near DArT marker bPb-2328 in 7HL (6); *sdw4.ba* is associated with SNP markers 1_1243 to 2_1363 (positions 167.56 to 198.70 cM) in 7H bins 10 to 12 of the Bowman backcross-derived line BW831 (1); likely in 7H bin 11.

Description:

Semidwarf 4 (*sdw4*) is a monofactorial recessive that reduces culm length by about 20 to 30% (4, 6) by affecting the length of the 3rd and 4th culm internodes proportional more than the upper internodes (3, 4). The *sdw4* gene was associated with reduced lodging (4). Combining *sdw4* with *uzu1* (*uzu* 1) reduced plant height further (3). In the Bowman backcross-derived line for *sdw4.ba* (BW831), plants were shorter, but the culms were slightly more robust and the flag leaves were larger than those of Bowman. Delayed heading was observed in plants with the *sdw4.ba* gene in some genetic backgrounds (2). The *sdw4.ba* mutation in China was reported to have originated as dwarf mutant (68-142) induced in the late 1960s by gamma-rays in the Chinese landrace Zhenongguangmangerleng (7). The first cultivar containing this mutant was Zhepi 1, released in 1978 by the Zhejiang Academy of Agricultural Science (7). Most cultivars now grown in the lower valley of Yangtze River were selected from crosses to Zhepi 1 (7).

Origin of mutant:

A gamma-ray induced mutant in the Chinese landrace Zhenongguangmangerleng (6); a spontaneous variant in the Japanese cultivar Kanto Nakate Gold (OUJ 518) released in 1953 (4), both parents of Kanto Nakate Gold, Shikoku (OUJ 546) and Golden Melon (OUJ808. PI 263410) are tall cultivars (4, 5).

Mutational events:

sdw4.ba (68-142) in Zhenongguangmangerleng (6), in the Japanese cultivar Kanto Nakate Gold (OUJ 518, PI 383933) (4). Based on morphological traits and chromosomal location of mutant, both mutational events are very similar.

Mutant used for description and seed stocks:

sdw4.ba in Zhepi 1 and Zhenongda 7; *sdw4.ba* in Kanto Nakate Gold (OUJ 518, PI 383933); *sdw4.ba* from Zhenongda 7 in Bowman*2 (BW831, NGB 22268).

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Prepared:

J.D. Franckowiak and G.T. Yu. 2011. Barley Genet. Newsl. 41:80-81.

BGS 61, Triple awned lemma 1, *trp1*

Stock number: BGS 61
Locus name: Triple awned lemma 1
Locus symbol: *trp1*

Previous nomenclature and gene symbolization:

Triple-bearded variation (5).
Triple awned lemma = *tr* (4).

Inheritance:

Monofactorial recessive (4).
Located in chromosome 4HL (2), *trp1.a* is associated with SNP markers 2_1397 to 1_0467 (positions 47.8 to 105.27 cM) in 4H bins 05 to 07 of the Bowman backcross-derived line BW881 (2), likely in 4H bin 07. Previously located in chromosome 2HL (4, 7), over 35.5 cM distal from the *wst7* (white streak 7) locus (1), but the *wst7* locus is in a subterminal position in 2HL (2), near AFLP marker E3644-13 in subgroups 22 and 23 of the Proctor/Nudinka map (6).

Description:

Mutants may have three awns on the lemma instead of one, but expression is variable (5). The awn or hood extending from the lemma of the central spikelet forks to form one normal central appendage and one or two shorter lateral ones (4). Expression of triple awn trait in the Bowman backcross-derived line BW881 is reduced to an occasional branch in the basal part of the awn. . However, when plants are grown under heat stress a stronger expression of the *trp1* trait was observed. Other morphological deviations from Bowman were not observed (3). The conflict in chromosome map positions suggests that strong expression of the triple awn phenotype may involve two loci (3).

Origin of mutant:

A spontaneous mutant in an unknown cultivar (5), possibly of natural occurrence in six-rowed cultivars originating from East Asia (3).

Mutational events:

trp1.a in Triple-awn lemma (Clho 6630, GSHO 210) (5).

Mutant used for description and seed stocks:

trp1.a in Clho 6630 (GSHO 210); *trp1.a* from Clho 6880 (Ahang/Twisted Flag//Triple-awn Lemma) in Bowman (PI 483237)*7 (GSHO 1936, BW881, NGB 22315).

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Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:97.

J.D. Franckowiak 2011. Barley Genet. Newsl. 41:82-83.

BGS 75, Awnless 1, *Lks1*

Stock number: BGS 75
Locus name: Awnless 1
Locus symbol: *Lks1*

Previous nomenclature and gene symbolization:

Awnless = *I* (Ikeno, see 3).
Awnless = *Lk* (4).
Awnless = *S* (8).
Two-rowed awnless = V^{lk} (12).

Inheritance:

Monofactorial dominant (3, 4, 7).
Located in chromosome 2HL (3, 4), about 9.6 cM distal from the *vrs1* (six-rowed spike 1) locus (8); *Lks1.a* is associated with SNP markers 1_0619 to 1_1533 (positions 133.59 to 141.56 cM) in 2H bins 09 to 10 of the Bowman backcross-derived line BW490 (2); *Lks1.b* is associated with SNP markers 2_0667 to 1_0287 (positions 117.73 to 138.37 cM) in 7H bins 08 to 09 of the Bowman backcross-derived line BW491 (2), likely in 2H bin 09.

Description:

Little or no development of the appendage on the lemma occurs. Heterozygotes may be awnless (1) or awnletted (4) depending upon the source stock for the *Lks1* gene and the genetic background. The *Lks1.a* allele in Engleawnless will not recombine with alleles at the *vrs1* (six-rowed spike 1) locus (4, 13) because a short paracentric inversion is present in Engleawnless (14). The complex *vrs1* locus may include awnless and reduced awn length mutants (13). However, the *Lks1.b* gene in Clho 13311 does recombine with *vrs1* locus and is associated with a dominant instead of a recessive allele at the *Gth* (toothed lemma) locus (5). In the Atlas near-isogenic lines, the awnless trait reduced kernel weight by about 15% (9, 11) and grain yield by about 10% (9, 10, 11). Both backcross-derived lines, BW490 with *Lks1.a* and BW491 with *Lks1.b*, are slightly taller than Bowman. The kernels of BW490 are longer and thinner than those of Bowman and weighed about 25% less. The kernels of BW491 are similar in size to those of Bowman and weighed 5 to 10% less (5).

Origin of mutant:

Natural occurrence in Engleawnless or *Hordeum inerme* (Clho 2505, PI 174480) (3, 4); and several other accessions (4, 8).

Mutational events:

Lks1.a in Engleawnless (Clho 2505, GSHO 44) from England (1, 12, 14); *Lks1.b* in Clho 13311 (PI 316871, GSHO 1579) from Ethiopia; the dissimilar SNP marker haplotypes in the critical region of 2H suggests that the *Lks1* variants are of independent origin (2).

Mutant used for description and seed stocks:

Lks1.a in Engleawnless (GSHO 44); *Lks1.b* in Clho 13311 (PI 316871, GSHO 1579); *Lks1.a* from Clho 2505 in Betzes (PI 129430)*7 (PI 534510); *Lks1.a* in Compana (PI 537442)*7 (PI 534512), *Lks1.a* in Dekap (Clho 3351)*7 (PI 534514), *Lks1.a* in Ingrid (Clho 10083)*7 (PI 534516, Ridawn) (4); *Lks1.a* from Ridawn in Bowman (PI 483237)*5 (GSHO 1913), in Bowman*6 (BW490, NGB 20718); *Lks1.b* from Clho 13311 in Bowman*6 (GSHO 1912), in Bowman*7 (BW491, NGB 20719).

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Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:84-85.

BGS 78, Mottled leaf 4, *mtt4*

Stock number: BGS 78
Locus name: Mottled leaf 4
Locus symbol: *mtt4*

Previous nomenclature and gene symbolization:

Mottled leaf-e = *mt_e*, *e* (3).

Mottled leaf = *mt* (6).

Inheritance:

Monofactorial recessive (3, 4, 5).

Located in chromosome 2HL (3, 5); about 13.7 cM distal from the *vrs1* (six-rowed spike 1) locus (3, 5); *mtt4.e* is associated with SNP markers 2_1340 to 2_0182 (positions 166.06 to 185.53 cM) in 2H bins 11 to 12 of the Bowman backcross-derived line BW602 (1), likely in 2H bin 11.

Description:

When the plants are grown under cool conditions, white-yellowish blotches develop as horizontal bands in seedling leaves, 2 to 4 per leaf blade (3). The bands faded as the plant grows or under warmer environmental conditions. At later stages of development, plants had a slightly yellow-green color (2). Plants of the Bowman backcross-derived line for *mtt4.e*, BW602, headed a few days later than Bowman, had 2 to 3 more kernels per spike, were slightly shorter, had slightly lighter kernel weights. The grain yields of BW602 were similar to those of Bowman (2).

Origin of mutant:

A spontaneous mutant in Victorie (OUU010, Clho 5077) (3).

Mutational events:

mtt4.e (OUL076, GSHO 1231) in Victorie (3).

Mutant used for description and seed stocks:

mtt4.e in Victorie (GSHO 1231, OUL076); *mtt4.e* in Bowman (PI 483237)*6 (GSHO 1914), in Bowman*7 (BW602, NGB 22168).

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Prepared:

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Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:86.

BGS 79, White streak 7, *wst7*

Stock number: BGS 79
Locus name: White streak 7
Locus symbol: *wst7*

Previous nomenclature and gene symbolization:

Ribbon grass = *rb* (7).
White streak-k = *wst_k* (11).
White streak-B = *wst_B* (9).

Inheritance:

Monofactorial recessive (2, 12).
Located in chromosome 2HL (6, 8, 9, 10); about 22.0 cM distal from the *gpa1* (grandpa 1) locus (2, 10); over 29.4 cM distal from the *lig1* (liguleless 1) locus (9); about 6.1 cM from RFLP marker MWG949A (1); *wst7.k* is associated with SNP markers 2_1346 and 1_283 (positions 233.94 and 234.63 cM) in 2H bin 14 of the Bowman backcross-derived line BW916 (3), in 2H bin 14.

Description:

Vertical white streaks of variable width and number develop in the leaf blades of young secondary tillers. Fewer white streaks and fewer tillers with white streaks occur as environmental conditions become warm. White streaks can be found until near maturity, but they are difficult to observe after heading under field conditions. Often the lower or first leaves on early tillers have more and wider streaks. There were no apparent effects of the *wst7.k* gene on agronomic traits in the Bowman backcross-derived line BW916 (5).

Origin of mutant:

A spontaneous mutant isolated by Robertson (7, 12).

Mutational events:

wst7.k (GSHO 247) in an unknown cultivar (2, 12).

Mutant used for description and seed stocks:

wst7.k in an unknown cultivar (GSHO 247); *wst7.k* from R.I. Wolfe's Multiple Recessive Marker Stock (GSHO 3451) in Bowman (PI 483237)*7 (GSHO 1935, BW916, NGB 22347).

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Prepared:

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Revised:

J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:207-208.

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:87-88.

BGS 82, Zeocriton 1, *Zeo1*

Stock number: BGS 82
Locus name: Zeocriton 1
Locus symbol: *Zeo1*

Previous nomenclature and gene symbolization:

Erectoides-52 = *ert-52* (6, 7).

Erectoides-r = *Ert-r* (10).

"Kurz und dicht" = *Knd* (14).

Inheritance:

Monofactorial incomplete dominant (6, 11).

Located in chromosome 2HL (9), about 9.2 cM distal from the *lig1* (liguleless 1) locus (9); about 7.3 cM distal from RFLP marker *cnx1* in 2H bin 13 (1); the *Ert-r.52* allele in Bowman backcross-derived line BW322 is associated with SNP markers 2_0715 to 1_0551 (positions 213.08 to 221.70 cM) in 2H bin 13 (2); the *Zeo1.a* allele in BW937 is associated with SNP markers 2_0715 to 2_1453 (positions 213.08 to 245.71 cM) in 2H bin 13/14 (2); the *Zeo1.b* allele in BW938 is associated with SNP markers 1_1486 to 2_0590 (positions 202.70 to 218.47) in 2H bin 13 (2), likely in 2H bin 13.

Description:

Plants heterozygous for *Zeo1* have short culms, compact spikes, and wide kernels. Homozygotes have shorter culms (short peduncle), very compact spikes, large outer glumes with long awns, and reduced fertility (14). Generally, the spike emerges from the side of the sheath in homozygotes. Although the name *zeocriton* is used for this gene, this gene is not from Spratt, the dense ear type described by Engledow (3) or those described by Hayes and Harlan (8). Spikes of plants with the *Ert-r.52* mutant are compact in heterozygotes and very compact in homozygotes, with rachis internode length values from 1.4 to 1.8 mm. Homozygotes are about 2/3 normal height with excellent vigor. The glumes associated with lateral spikelets are 3 to 4 times larger than normal. Lodicule size is reduced (11). Heterozygotes are intermediate in plant height, have slightly more lax spikes, and have normal glumes in lateral spikelets (11). GA₃ treatment of plants as the flag leaf emerges decreases spike density (13). Plants in Bowman backcross lines for *Ert-r.52* (BW322), *Zeo1.a* (BW937), and *Zeo1.b* (BW938) are about 2/3 the height of Bowman. Rachis internodes are about 1/2 normal length (2.2 vs. 4.4 mm). Mutant plants head about two days later than Bowman; they have about 2 more kernels per spike and their grain yields are about 3/4 of those of Bowman. Plants with *Ert-r.52* mutant appeared slightly less stunted than those with *Zeo1.a* or *Zeo1.b* (5). The *Zeo1* locus is very close to the *Zeo2* locus (2, 5).

Origin of mutant:

An X-ray induced mutant in Donaria (PI 161974) (12); a neutron induced mutant in Bonus (PI 189763) (6).

Mutational events:

Zeo1.a in Donaria (Mut 2657, GSHO 1613) (12); *Zeo1.b*, received as "Kurz und dicht" and placed in R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 1614) (4, 14); *Ert-r.52* (NGB 112651, GSHO 492), *-r.67* (NGB 112666) in Bonus, *-r.329* (NGB 112844) in Foma (Cihó 11333) (11); *Ert-r.453* (NGB 112968) in Foma (10).

Mutant used for description and seed stocks:

Zeo1.a in Donaria (GSHO 1613); *Zeo1.a* in Bowman (PI 483237)*5 (GSHO 1931), in Bowman*7 (BW937, NGB 22366); *Zeo1.b* from R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 1614) in Bowman*9 (GSHO 1932, BW938, NGB 22367); *Ert-r.52* in Bonus (GSHO 492, NGB 112651); *Ert-r.52* in Bowman (PI 483237)*8 (GSHO 2123, BW322,

NGB 22117).

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Prepared:

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U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:280. as BGS 332, Erectoides-r, *Ert-r*.

Revised:

- J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:209.
J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:89-90.

BGS 93, Erectoides-zd, *ert-zd*

Stock number: BGS 93
Locus name: Erectoides-zd
Locus symbol: *ert-zd*

Previous nomenclature and gene symbolization:

Erectoides-159 = *ert-159* (5).

Brachytic 7 = *br7* (6).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 7HL (1); *ert-zd.159* is associated with SNP markers 1_0547 and 3_0166 (about position 232 cM) in 7H bin 14 of the Bowman backcross-derived line BW333 (1). Previously located in chromosome 2H, based on linkage drag with the *Gth1* (toothed lemma 1) locus (4).

Description:

Plants have a brachytic-like pattern of growth and are about 3/4 normal height (3, 6).

The basal rachis internode was slightly elongated. Plants of BW333, the Bowman backcross-derived line for mutant *ert-zd.159*, were 10 to 20% shorter than Bowman and the awns were about 3 cm shorter. Rachis internode lengths were slightly shorter and kernels were slightly wider for BW333 compared to those of Bowman. Kernel weights varied from slightly more to 15% less. Grain yields for BW333 varied from 1/3 to 1/2 those for Bowman (2).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (5).

Mutational events:

ert-zd.159 (NGB 112758, GSHO 504) in Bonus (5).

Mutant used for description and seed stocks:

ert-zd.159 in Bonus (GSHO 504, NGB 112758); *ert-zd.159* in Bowman (PI 483237)*7 (GSHO 1901, BW333, NGB 22128).

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:132.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:91.

BGS 99, Lesser internode number 1, *lin1*

Stock number: BGS 99
Locus name: Lesser internode number 1
Locus symbol: *lin1*

Previous nomenclature and gene symbolization:

Rachis internode number = *s*, *rin* (3, 6).
Low number of rachis internodes = *rin* (4).
Rachis internode length QTL on 2H = *qSIL.ak-2H* (5).

Inheritance:

Monofactorial recessive (6, 7).
Located in chromosome 2HS (7); about 15.1 cM distal from the *eog1* (elongated outer glume 1) locus and about 17.1 cM proximal from the *vrs1* (six-rowed spike 1) locus (6); about 6 cM proximal from STS marker ABG602 and the *Eam1* (early maturity 1) locus (5), likely in 2H bin 06.

Description:

The mean number of rachis internodes per spike is reduced by 20 to 40% (6, 7). The average internode number was 15.3 in Triple Bearded Mariout and 22.9 in Spartan (6). Presence of the *Eam1* (early maturity 1) gene closely linked to *lin1.a* gene in Triple Bearded Mariout (BGS 57) made study of *lin1* locus difficult in some environments; therefore, a new BGS number was recommended (2). In some six-rowed cultivars such as Morex, the reduction in rachis internodes associated with the *lin1* gene is less obvious (1). A significant reduction triplet number, 1.5 to 2.3 fertile rachis nodes, was associated with the Azumamugi allele in 2HS and mapped near the *Eam1* (early maturity 1) locus (5). Since mapping population was grown under short-day conditions, the effects of the *Eam1* gene on maturity and plant development were not expressed (5). The effects of alleles at the *lin1* locus on fertile rachis nodes are more obvious when barley is grown in heat stressed environments. Fewer fertile rachis nodes per spike may lead to plumper kernels. The *lin1.a* gene is likely present in Bowman and may be associated with its increased tolerance to heat stress (1).

Origin of mutant:

Natural occurrence in many six-rowed barley cultivars of North African and Asian origin (1). (Tavcar's mutant stock is no longer available).

Mutational events:

lin1.a in Triple Bearded Mariout (CIho 2523, GSHO 29) (6).

Mutant used for description and seed stocks:

lin1.a in Morex (CIho 15773, GSHO 2492); *lin1.a* from Nordic (CIho 15216) in Bowman (PI 483237).

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Prepared:

T. Tsuchiya and T.E. Haus. 1971 Barley Genet. Newsl. 1:117 as BGS 57, Reduced internode number, *rin*.

Revised:

T. Tsuchiya and T.E. Haus. 1984. Barley Genet. Newsl. 14:91 as BGS 57, Lesser internode number, *lin*.

J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:88: BGS number changes from BGS 57 to BGS 99.

J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:92-93.

BGS 102, Uzu 1, *uzu1*

Stock number: BGS 102
Locus name: Uzu 1 (semi-brachytic)
Locus symbol: *uzu1*

Previous nomenclature and gene symbolization:

Normal vs *uzu* = *h* (16).
Uzu = *u* (7).
Uzu (semi-brachytic) = *uz* (15).
Uzu 2 = *uz2* (17, 19).
Uzu 3 = *uz3* (17, 19).
Hordeum vulgare BR-insensitive 1 = *HvBRI1* (1).

Inheritance:

Monofactorial recessive (7, 11, 13, 15).
Located in chromosome 3HL (9, 10, 15); about 17.6 cM proximal from the *alm1* (albino lemma 1) locus (13); in bin 3H-06 near cDNA marker C1271 (1); about 10.1 cM from AFLP marker E3733-6 in subgroup 27 of the Proctor/Nudinka map (8), *uzu1.a* is associated with SNP markers 1_0373 to 1_1314 (positions 92.55 to 107.40 cM) in 3H bins 06 to 07 of the Bowman backcross-derived line BW885 (2); *uzu1.a* with *sld1.a* is associated with SNP markers 1_0653 to 2_0115 (positions 92.55 to 126.83 cM) in 3H bins 06 to 08 of the Bowman backcross-derived line BW860 (2); *uzu1.a* with *wst1.c* is associated with SNP markers 1_1258 to 2_0155 (positions 79.88 to 229.92 cM) in 3H bins 05 to 15 of the Bowman backcross-derived line BW912 (2); BW860, BW885, and BW912 have a common SNP marker pattern from 1_1191 to 2_0931 (positions 98.41 to 104.39 cM) in 3H bin 06 (2), in 3H bin 06.

Description:

The *uzu1.a* gene has pleiotropic effects on the elongation of the coleoptile, leaf, culm, rachis internode, awn, glume, and kernel (12, 13, 15). These organs are often reduced in length and increased in width. Changes in organ length are temperature sensitive, but heading date and maturity are unaltered. Coleoptile of *uzu* plants shows a prominent projection or hook near the apex. Sometimes the coleoptile of the mutant shows a V-shaped notch on the side opposite from the projection. Thus, the apex of the coleoptile has two notches, one on each side (13, 17, 18). The temperature sensitive reduction in culm length of *uzu1.a* plants ranged from less than 15% in cool environments to over 75% in warm ones. The Bowman backcross-derived line for *uzu1.a*, BW885, produced plants that were 20 to 40% shorter than Bowman, awns were about 1/3 of normal length, rachis internodes were shorter, 3.0 vs. 4.7 mm, and leaf blades were shorter and wider. Kernels of BW885 were shorter, 7.9 vs. 9.5 mm, and lighter, averaged 4.7 vs. 5.7 mg. Spikes of BW885 often had 2 more kernels than those of Bowman. Grain yields of BW885 ranged from 1/3 to 3/4 those of Bowman (3). Chono et al. (1) reported that the *uzu1.a* or *HvBRI1* gene is caused by a mutation that changed a highly conserved residue of the kinase domain of *BRI1* (*Arabidopsis* BR-insensitive 1) (brassinosteroids) receptor protein from His-857 to Arg-857. A second mutant in the *HvBRI1* gene was identified by Gruszka et al. (5).

Origin of mutant:

Natural occurrence in many cultivars of Japanese origin (12, 13).

Mutational events:

uzu1.a (OUJ371, PI 182624, GSHO 1300) in many Japanese cultivars (13, 17, 19);
uzu1.b (092AR) in Aramir (PI 467781) (4, 5).

Mutant used for description and seed stocks:

uzu1.a (OUJ371, PI 182624, GSHO 1300) in Baitori 11; *uzu1.a* in Bowman (PI 483237)*7 (GSHO 1963, BW885, NGB 20787); *uzu1.a* with *wst1.c* (OUL074, GSHO 569) from Akashinriki (PI 467400, OUJ659) in Bowman*8 (GSHO 1967, BW912, NGB 22348); *uzu1.a* with *sld1.a* (OUM148, GSHO 2489) from Akashinriki in Bowman*8 (GSHO 1971, BW860, NGB 22397).

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Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:124.

Revised:

T. Tsuchiya. 1984. Barley Genet. Newsl. 14:92.

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:136-137.

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:220-221.

J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:94-96.

BGS 107, White steak 1, *wst1*

Stock number: BGS 107
Locus name: White streak 1
Locus symbol: *wst1*

Previous nomenclature and gene symbolization:

White stripe = *wst* (5).
Stripe = *st* (3, 6).
White streak 3 = *wst3* (8, 9, 10, 12, 13).

Inheritance:

Monofactorial recessive (3, 6, 10).
Located in chromosome 3HL (5, 7, 9, 14); very close to the *uzu1* (*uzu* 1) locus (3, 8, 9, 13); *wst1.a* is associated with SNP markers 2_0968 to 1_0584 (positions 46.19 to 178.12 cM) in 3H bins 04 to 11 of the Bowman backcross-derived line BW910 (1); *wst1.c* with *uzu1.a* is associated with SNP markers 1_1258 to 2_0155 (positions 79.88 to 229.92 cM) in 3H bins 05 to 15 of the Bowman backcross-derived line BW912 (1).

Description:

Very narrow white stripes are present in the leaves from the seedling stage until near maturity. Plants have nearly normal vigor (5). The size of the white sectors is variable from mutant to mutant, plant to plant, and leaf to leaf. All affected plants may produce albino seedlings among their selfed progeny with reported frequencies between 1.0 and 25.6% (9, 11). Albino seedlings have not been observed when *wst1* plants were used as the male parent in crosses (9, 11). Caldecott's streak has wider and larger white sectors and produces a higher frequency of albino seedlings (11). Compared to Bowman, plants of the Bowman backcross-derived line for *wst1.a*, BW910, headed 3 to 4 days later and were slightly shorter, but the awns were slightly longer. The kernels of BW910 were slightly narrower, 3.7 vs. 3.9, and lighter than the Bowman kernels in many trials. The test weights and grain yields for BW910 were slightly reduced (2).

Origin of mutant:

A spontaneous mutant in an unknown cultivar (3, 8, 11); a radiation induced mutant (8, 9, 10, 11, 12).

Mutational events:

wst1.a (USDA 163, Clho 11767, GSHO 159) in an unknown cultivar (4); *wst1.c* (OUL074, GSHO 569) in Akashinriki (PI 467400, OUJ659) (9, 10, 11, 12); *wst1.e* in Himalaya (GSHO 278, Caldecott's streak) (10, 14); *wst1.f* (Grandpa fine stripe) in an unknown cultivar (Clho 6856, GSHO 854), *wst1.g* in Clho 6758 (GSHO 314) (10); *wst1.h* in Clho 11766 (GSHO 797) (4, 10); *wst1.i* in Moravian (PI 537135) (10).

Mutant used for description and seed stocks:

wst1.a in an unknown cultivar (GSHO 159, Clho 11767); *wst1.a* in Bowman (PI 483237)*6 (GSHO 1966), in Bowman*7 (BW910, NGB 22341); *wst1.c* with *uzu1.a* (OUL074, GSHO 569) from Akashinriki (PI 467400, OUJ659) in Bowman*8 (GSHO 1967, BW912, NGB 22343).

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Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:129.

Revised:

T. Tsuchiya. 1980. Barley Genet. Newsl. 10:110.

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:141-142.

J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:97-98.

BGS 111, Dense spike 10, *dsp10*

Stock number: BGS 111
Locus name: Dense spike 10
Locus symbol: *dsp10*

Previous nomenclature and gene symbolization:

Dense spike $c = I_c$ (6, 8).

Inheritance:

Monofactorial recessive (2, 8).

Located in chromosome 3HL (2, 5, 8), about 1.3 cM distal from the *xnt3* (xantha seedling 3) locus (7, 8.); *dsp10.c* is associated with SNP markers 2_0002 to 1_0628 (positions 82.03 to 135.80 cM) in 3H bins 05 to 07 of the Bowman backcross-derived line BW278; *dsp10.ai* (previously *pyr.ai*) is associated with SNP markers 2_1109 to 2-1305 (positions 78.82 to 103.33 cM) in 3H bins 05 to 06 of the Bowman backcross-derived line BW655; *dsp10.aj* (previously *dsp.aj*) is associated with SNP markers 2_0794 to 1_0747 (positions 39.80 to 144.30 cM) in 3H bins 04 to 09 of the Bowman backcross-derived line BW258 (1); the region of 3H with common SNP markers retained all three stocks is from 2_002 to 1_0224 (positions 82.03 to 85.26) (1, 3), in 3H bin 05 near the centromere. A small common set of SNP markers 2_002 to 1_0925 (positions 82.03 to 84.19 cM) are preserved in dense spike variants from Steptoe: *dsp10.ba* (BW273), *dsp10.bb* (BW274), and *dsp10.bc* (BW275) (1, 3).

Description:

Although rachis internode length or spike density is not a highly stable character, plants with relatively dense spikes can be selected from crosses to Club Mariout. Rachis internode length values of 2.8 to 3.4 mm, 2.9 to 3.6 mm, and 2.6 to 2.8 mm were recorded for Club Mariout in one experiment (8). Plants in Bowman backcross-derived lines for *dsp10* locus (BW258, BW278, and BW655) had average rachis internode lengths of 3.3 mm compared to 4.6 mm for Bowman. The plants were 5 to 15% shorter than Bowman plants and spikes averaged 2 to 3 more kernels. Kernel weights and grain yields of the Bowman lines with *dsp10* were similar to values for Bowman (3).

Origin of mutant:

Natural occurrence in Club Mariout (CIho 261, PI 9877) (2, 8) and other cultivars (9).

Mutational events:

dsp10.c in Club Mariout (CIho 261, GSHO 71) (2, 8).

Mutant used for description and seed stocks:

dsp10.c in Club Mariout (GSHO 71, CIho 261, PI 9877); *dsp10.c* in Bowman (PI 483237)*3 (GSHO 1956), in Bowman*6 (BW278, NGB 20562); *dsp10.ai* from a 6-rowed line mutated in Sweden (18:08:04, GSHO 2433) (4) in Bowman*6 (GSHO 2241), in Bowman*7 (BW655, NGB 22220); *dsp10.aj* from a 6-rowed line mutated in Sweden (18:08:04, GSHO 1720) (4) in Bowman*5 (GSHO 2242), in Bowman*6 (BW258, NGB 22083); *dsp10.ba* from UT1713 (GSH1730) in Bowman*6 (GSHO2251), in Bowman*7 (BW273, NGB 22098); *dsp10.bb* from Steptoe mutant (Az34, GSHO2415) in Bowman*3 (BW274, NGB 22099); *dsp10.bc* from Steptoe mutant (FN4) in Bowman*4 (BW275, NGB 22100).

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Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:133.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:145.

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:99-100.

BGS 124, Six-rowed spike 4, *vrs4*

Stock number: BGS 124
Locus name: Six-rowed spike 4
Locus symbol: *vrs4*

Previous nomenclature and gene symbolization:

Multiflorus = *mul* (8, 17).
Intermedium spike-e = *int-e* (6, 11).
Six-rowed spike 4 = *v4* (3).

Inheritance:

Monofactorial recessive (3, 4, 5, 7).
Located in chromosome 3HL (5, 14, 15, 16), but the arm designation was later reversed (16); about 27.5 cM from the *uzu1* (*uzu* 1) locus (5); *int-e.58* is associated with SNP markers 1_0672 to 2_1083 (positions 38.56 to 156.06 cM) in 3H bins 04 to 10 of the Bowman backcross-derived line BW423 (1); *mul1.a* is associated with SNP markers 1_0762 and 2_0115 (positions 38.56 and 126.83 cM) in 3H bins 04 and 08 of line BW606 (1); *vrs4.k* is associated with SNP markers 1_0863 to 1_0926 (positions 64.85 to 85.26 cM) in 3H bin 05 and with SNP markers 2_1493 to 1_1330 (positions 161.43 to 178.12 cM) in 3H bin 10 of the Bowman backcross-derived line BW903 (1); the lack of SNP marker heterogeneities in the centromeric region of the BW lines and more markers retained in 3HS indicate that the *vrs4* locus is more likely in 3H bin 05 (1, 2).

Description:

Alleles at this locus enhance the development of lateral spikelets and formation of additional spikelets to various degrees. The *int-e* mutants, which were isolated in two-rowed cultivars, have enlarged lateral spikelets that may set seed in the upper two-thirds of the spike. Kernels in lateral spikelets are smaller than those from central spikelets in *int-e* mutants. The rachilla may be deformed by partial formation of an extra spikelet. The awn size on lateral spikelets ranges from a pointed apex to 3/4 normal length (12). The *mul1.a* and *vrs4.k* alleles, which were isolated in six-rowed cultivars, may produce numerous extra spikelets at the base of the lateral spikelets and on the rachilla (4, 8). Plants of the backcross derived line BW903 with the *vrs4.k* allele and BW606 with *mul1.a* are slightly taller than Bowman, plants lodge easily, and rachis internodes are slightly longer. Kernels of BW423 with *int-e.58* had weights that range similar to those of Bowman to 10% less. Kernels of BW606 and BW903, which include small lateral ones, had average weights 20 to 40% less than those of Bowman. The kernel weights for BW606 were slightly less than those of BW093. Kernels of all BW lines with *vrs4* alleles were about 10% shorter than those of Bowman (2).

Origin of mutant:

A gamma-ray induced mutant in MFB 104 (PI 232921) (5).

Mutational events:

mul1.a (Alb Acc 321, GSHO 561) in Montcalm (Clho 7149) (8, 17); *vrs4.k* (Gamma III 3B, MFB-2, GSHO 775) in MFB 104 (PI 232921), *vrs4.l* (Xc 41.5, Piro-2) in Pirolino (PI 262210) (5); *vrs4.m* (X17 2497, Piro-7) in Pirolino (4, 5); *int-e.4* (trans) (NGB 115212) in Bonus (PI 189763), -e.20 (trans) (NGB 115438), -e.23 (NGB 115441), -e.26 (NGB 115444) in Foma (Clho 11333), -e.58 (NGB 115476, GSHO 1776), -e.66 (NGB 115484) in Kristina (NGB 1500), -e.65 (NGB 115483) in Bonus (11); *int-e.72* (NGB 115490), -e.87 (NGB 115505) in Bonus, -e.89 (NGB 115507), -e.90 (NGB 115508), -e.91 (NGB 115509), -e.92 (NGB 115510), -e.101 (NGB 115519) in Hege (10); *hex-v.46* (NGB 115583), *hex-v.47* (NGB 115584), *hex-v.48* (NGB 115585) (9, 10).

Mutant used for description and seed stocks:

vrs4.k in Gamma III 3B (GSHO 775); *int-e.58* in Kristina (GSHO 1776); *mul1.a* in Bowman (PI 483237)*6 (GSHO 1985), in Bowman*7 (BW606, NGB 22172); *vrs4.k* in Bowman*6 (GSHO 1986), in Bowman*7 (BW903, NGB 22335); *int-e.58* in Bowman*6 (GSHO 1987), in Bowman*7 (BW423, NGB 20658).

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:159-160.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:101-102.

BGS 126, Slender dwarf 1, *sld1*

Stock number: BGS 126
Locus name: Slender dwarf 1
Locus symbol: *sld1*

Previous nomenclature and gene symbolization:

Dwarf 1 = *dw1* (3).

Light green dwarf = *dw-1* (8).

Inheritance:

Monofactorial recessive (4, 9).

Located in chromosome 3HL (6, 8, 9); over 6.3 cM distal from the *uzu1* (*uzu 1*) locus (6, 8); about 20.5 cM distal from the *uzu1* locus (8); about 1.2 cM from AFLP marker E3634-8 in subgroup 27 of the Proctor/Nudinka map (7); *sld1.a* is associated with SNP markers 2_1402 to 2_0362 (positions 77.00 to 119.10 cM) in 3H bins 05 to 07 of the Bowman backcross-derived line BW859 (1); *sld1.a* with *uzu1.a* is associated with SNP markers 1_0653 to 2_0115 (positions 92.55 to 126.83 cM) in 3H bins 06 to 08 of the Bowman backcross-derived line BW860 (1); *sld1.c* is associated with SNP markers 2_1145 to 2_0093 (positions 65.96 to 127.91 cM) in 3H bins 05 to 08 of the Bowman backcross-derived line BW861 (1); BW859 and BW860 have a common SNP patterns from 2_0017 to 2_0362 (positions 106.46 to 119.10 cM) in 3H bin 07 (1), in 3H bin 07.

Description:

Plant height is reduced to about 1/2 to 2/3 of normal, plant development is delayed, and plants are slightly yellow green in color (3, 8). Plants of the mutant *sld1.a* (*dw-a*, OUM148) headed 4 days later and were shorter, 81 vs. 122 cm, than their parent, Akashinriki (5). Kernel weights and kernels per spike of *sld1.a* plants were reduced and grain yields were 30% lower (5). The distribution of leaves in *sld1* plants was altered because the peduncle is relatively long in proportion to the other internodes. Plants homozygous for the *sld1.c* allele were slightly weaker and shorter than *sld1.a* plants in their respective Bowman backcross-derived lines, BW861 and BW859 (2). Heading was delayed about 5 days in both BW859 and BW861. BW859 plants exhibited about 30% reduction in plant height, but had about 3 more kernels per spike. Kernel weights for BW859 were 5 to 15% lower than those of Bowman and grain yields ranged from 1/3 to 90% those of Bowman. Plants of BW861 showed a 40% reduction in plant height compared to Bowman, spikes had an average of 2 more kernels, kernel weights were 10 to 25% lower, and grain yield ranged from 10 to 75% those of Bowman (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (3).

Mutational events:

sld1.a (*dw-a*, OUM148, GSHO 2488) in Akashinriki (3, 6); *sld1.c* (862PK, GSHO 2489) in Plena (PI 321822) (2, 8).

Mutant used for description and seed stocks:

sld1.a in Akashinriki (GSHO 2488, OUM148); *sld1.a* in Bowman (PI 483237)*7 (GSHO 1970), in Bowman*8 (BW859, NGB 22296); *sld1.c* in Bowman*7 (GSHO 1972, BW861, NGB 22298); *sld1.a* with *uzu1.a* (OUM148, GSHO 2489) from Akashinriki in Bowman*8 (GSHO 1971, BW860, NGB 22297).

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Prepared:

T. Konishi and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:162.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:103-104.

BGS 129, White streak 6, *wst6*

Stock number: BGS 129
Locus name: White streak 6
Locus symbol: *wst6*

Previous nomenclature and gene symbolization:

White stripe j = *wst_j* (5).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 3HL (4, 5); about 10.6 cM distal from the *uzu1* (*uzu 1*) locus (3, 4, 5); *wst6.j* is associated with SNP markers 2_1305 to 2_0626 (positions 103.33 to 152.84 cM) in 3H bins 06 to 10 of the Bowman backcross-derived line BW915 (1), likely in 3H bin 07.

Description:

When grown under low temperature conditions, the leaf sheath and leaf blade become whitish or white streaked. In some cases, only the leaf tip and the central portion of the blade remained green (5). White streaks were not expressed above 20°C (5). A white streaked phenotype was expressed in seedlings grown under greenhouse conditions (2). Plants of BW915, the Bowman backcross-derived line for *wst6.j*, were up to 7 days later, 10 to 15 cm shorter, and lower yielding than Bowman in some environments. However, BW915 was similar Bowman in other field trials (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (5).

Mutational events:

wst6.j (OUM231, GSHO 2500) in Akashinriki (4, 5).

Mutant used for description and seed stocks:

wst6.j in Akashinriki (OUM231, GSHO 2500); *wst6.j* plus *uzu1.a* in Bowman (PI 483237)*3 (GSHO 1968); *wst6.j* in Bowman*7 (BW915, NGB 22346).

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Prepared:

J.D. Franckowiak and T. Konishi. 1997. *Barley Genet. Newsl.* 26:165.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:105.

BGS 132, Breviaristatum-a, *ari-a*

Stock number: BGS 132
Locus name: Breviaristatum-a
Locus symbol: *ari-a*

Previous nomenclature and gene symbolization:

Breviaristatum-6 = *ari-6* (3, 4).
Short awn 7 = *lk7* (9).

Inheritance:

Monofactorial recessive (4).
Located in chromosome 3HS (6, 7, 8); probably less than 2.4 cM from the centromere (7); *ari-a.6* is associated with SNP markers 2_1197 to 1_0653 (positions 78.82 to 92.55 cM) in 3H bins 05 to 06 of the Bowman backcross-derived line BW038 (1), likely in 3H bin 05.

Description:

A common feature of mutants at this locus is instability in the expression of awn length, ranging from very short to 5/6 normal length in various environments (4). In some environments, secondary or tertiary tillers may show a drastic reduction in the length of stem internodes, spikes, and awns. Awns are thin and brittle and may flare somewhat on later tillers. Kernels are thin with fine wrinkles on the lemma (4). Plants of BW038, the Bowman backcross-derived line for mutant *ari-a.6*, were 10 to 20% shorter than Bowman and their awns extended beyond the tip of the spike 5 to 9 cm vs. 11 to 12 cm for Bowman. Kernels of BW038 were slightly smaller in size and weighed 10 to 20% less than the Bowman kernels. Grain yields of BW038 were about 2/3 those of Bowman (2).

Origin of mutant:

A gamma-ray induced mutant in Bonus (PI 189763) (4).

Mutational events:

ari-a.6 (NGB 115850, GSHO 1648), *-a.7* (NGB 115851) in Bonus (4); *ari-a.8* (NGB 115852), *-a.23* (NGB 115871) in Bonus (5); *ari-a.26* (NGB 115874) in Bonus (4); *ari-a.31* (NGB 115880) in Bonus (5); *ari-a.37* (NGB 115887), *-a.48* (NGB 115900) in Bonus, *-a.118* (NGB 115930), *-a.121* (NGB 115933), *-a.124* (NGB 115936), *-a.126* (NGB 115938) in Foma (Clho 11333) (4); *ari-a.122* (NGB 115934), *-a.125* (NGB 115937), *-a.148* (NGB 115960) in Foma (5); *ari-a.152* (NGB 115962), *-a.162* (NGB 115972), *-a.174* (NGB 115984), *-a.211* (NGB 116020) in Foma (4); *ari-a.216* (NGB 116025) in Foma (5); *ari-a.273* (NGB 116085), *-a.277* (NGB 116090), *-a.279* (NGB 116092), *-a.287* (NGB 116104), *-a.293* (NGB 116113) in Kristina (NGB 1500) (4); *ari-a.296* (NGB 116116), *-a.305* (NGB 116131) in Kristina (5); *lks7.i* (Kmut 114) in Asahi 5 (OUJ509) (9).

Mutant used for description and seed stocks:

ari-a.6 in Bonus (GSHO 1648, NGB 115850); *ari-a.6* in Bowman (PI 483237)*7 (GSHO 1958, BW038, NGB 20446).

References:

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:168.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:106-107.

BGS 134, Erectoides-c, *ert-c*

Stock number: BGS 134
Locus name: Erectoides-c
Locus symbol: *ert-c*

Previous nomenclature and gene symbolization:

Erectoides-1 = *ert-1* (4).

Inheritance:

Monofactorial recessive (7, 8).

Located in chromosome 3HL (6, 12, 13), about 3.7 cM from the centromere (10, 11), and about 2.9 cM proximal from the *msg5* (male sterile genetic 5) locus (2); *ert-c.1* is associated with SNP markers 1_0380 to 2_1513 (positions 78.82 to 166.78 cM) in 3H bins 05 to 10 and with SNP markers 1_1302 to 2_1110 (positions 86.79 to 109.78 cM) in 2H bins 07 to 08 of the Bowman backcross-derived line BW305 (1).

Description:

Spikes have a compact or semi-compact appearance caused by a reduction in rachis internode length, with values from 1.7 to 2.9 mm (5, 12). The spike has a pyramid shape with shorter rachis internodes at the base and longer ones near the apex. The culm length is also highly variable among mutants at the *ert-c* locus. Mutants *ert-c.66* and *ert-c.153* are partially sterile, much shorter in culm length, and have a more bushy growth pattern than other mutants at this locus (5, 12). GA₃ treatment of plants as the flag leaf emerges decreases spike density (14). The Bowman backcross-derived line for *ert-c.1* (BW305) has a translocation between 2HL and 3HL based on retained SNP markers (1). Plants of BW305 were slightly later and taller than Bowman plants. Rachis internode lengths for BW305 averaged 3.4 vs. 4.6 mm and spikes had 5 to 7 more fertile rachis internodes (3). Compared to Bowman, BW305 had similar kernel weights and grain yields (3).

Origin of mutant:

An X-ray induced mutant in Gull (CIho 1145, GSHO 466) (4, 7, 8).

Mutational events:

ert-c.1 (trans) (NGB 112605, GSHO 471) in Gull (7, 15); *ert-c.14* (trans) (NGB 112615, GSHO 473) in Maja (PI 184884), -c.39 (NGB 112639), -c.47 (trans) (NGB 112646), -c.48 (NGB 112647), -c.59 (trans) (NGB 112658), -c.62 (NGB 112661), -c.66 (NGB 112665), -c.70 (trans) (NGB 112669), -c.75 (NGB 112674) (trans), -c.82 (NGB 112681), -c.83 (NGB 112682), -c.85 (NGB 112684), -c.88 (NGB 112687) in Bonus (PI 189763) (7); *ert-c.91* (NGB 112690), -c.95 (NGB 112694), -c.97 (NGB 112696), -c.98 (NGB 112697), -c.108 (NGB 112707), -c.137 (NGB 112736), -c.153 (NGB 112752), -c.173 (NGB 112774), -c.177 (NGB 112778) in Bonus (12); *ert-c.176* (NGB 112777), -c.179 (NGB 112780), -c.188 (NGB 112789) in Bonus (9); *ert-c.310* (NGB 112826), -c.311 (NGB 112827), -c.312 (NGB 112828) in Foma (CIho 11333) (12); *ert-c.320* (NGB 112835) in Foma (9); *ert-c.327* (NGB 112842), -c.342 (NGB 112858), -c.351 (NGB 112867) in Foma (12); *ert-c.352* (NGB 112868) in Foma (9); *ert-c.355* (NGB 112871), -c.369 (NGB 112885), -c.386 (NGB 112901), -c.395 (NGB 112912) in Foma (12); *ert-c.463* (NGB 112978) in Foma (9); *ert-c.495* (NGB 113011) in Foma (12).

Mutant used for description and seed stocks:

ert-c.1 in Gull (GSHO 471, NGB 112605); *ert-c.1* in Bowman (PI 483237)*7 (GSHO 1960, BW305, NGB 20587).

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:170-171.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:108-109.

BGS 172, Short awn 5, *lks5*

Stock number: BGS 172
Locus name: Short awn 5
Locus symbol: *lks5*

Previous nomenclature and gene symbolization:

Short awn 5 = *lk5* (7).
Breviaristatum-2 = *ari-2* (5, 6).
Breviaristatum-c = *ari-c.2* (6, 13, 14).

Inheritance:

Monofactorial recessive (6, 7).
Located in chromosome 4HL (15), about 6.9 cM distal from the *Kap1* (hooded lemma 1) locus (7, 9); near AFLP marker E4143-5 in subgroup 38 of the Proctor/Nudinka map (10); *lks5.f* is associated with SNP markers 1_0262 to 2_0072 (positions 76.26 to 95.92 cM) in 4H bin 06 of the Bowman backcrossed-derived line BW493 (2); *ari-c.2* is associated with SNP markers 2_0289 to 2_1322 (positions 69.62 to 112.64 cM) in 4H bins 05 to 08 of the Bowman backcrossed-derived line BW040 (2), in 4H bin 06; *lks5.p* isolated in genetic stocks BW474 and BW475 from the *le1* (lemma leafy 1) stock, G7118, *lks5.p* is associated with SNP markers 2_1122 to 1_1019 (positions 47.80 to 183.54) in 4H bins 05 to 13 of the Bowman backcrossed-derived line BW474 (2); *lks5.p* is associated with SNP markers 2_0422 to 2_0072 (positions 38.41 to 95.92 cM) in 4H bins 04 to 06 of the Bowman backcrossed-derived line BW475 (2).

Description:

Awns on both central and lateral spikelets are reduced to 1/4 or less of normal length in six-rowed cultivars (7). Only the central spikelets exhibit reduced awn length in two-rowed cultivars (3, 6). The rachilla is often modified, and in extreme cases the rachilla may develop as a malformed additional floret (7). Awns are thin and brittle (6). Plants of the Bowman backcross-derived line for *lks5.f*, BW493, had awns that extended 3 to 4 cm beyond the tip of the spike, while those of Bowman were 12 to 13 cm beyond the tip. Kernels of BW493 were slightly shorter, narrower (3.4 vs. 3.9 mm), and lighter (4.6 vs. 5.5 mg). BW493 plants were slightly taller than Bowman and grain yields were slightly reduced (4). Presence of the mutant allele *lks5.p* is needed for expression of the leafy lemma 1 (*le1.a*) gene (4, 10).

Origin of mutant:

A spontaneous mutant in an unknown cultivar (7).

Mutational events:

lks5.f (GSHO 1297) in Clho 5641 (7, 13); *lks5.g* (Kmut 218) in Asahi 5 (OUJ509) (13); *ari-c.2* (GSHO 1651, NGB 115847), -c.59 (NGB 115913) in Bonus (PI 189763), -c.103 (NGB 115915) in Foma (Clho 11333) (3); *ari-c.106* (NGB 115918) in Foma (5); *ari-c.109* (NGB 115921), -c.110 (NGB 115922), -c.111 (NGB 115923), -c.112 (NGB 115924), -c.120 (NGB 115932), -c.139 (NGB 115949), -c.157 (NGB 115967), -c.159 (NGB 115969), -c.179 (NGB 115989), -c.180 (NGB 115990), -c.199 (NGB 116008), -c.201 (NGB 116010), -c.203 (NGB 116012), -c.204 (NGB 116013), -c.206 (NGB 116014), -c.210a (NGB 116018), -c.210b (NGB 116019) -c.229 (NGB 116039) in Foma, -c.259 (NGB 116068), -c.262 (NGB 116071), -c.272 (NGB 116084), -c.276 (NGB 116089), -c.289 (NGB 116107), -c.291 (NGB 116111) in Kristina (NGB 1500) (6); *ari-c.307* (NGB 116135) in Kristina (8); two possible additional alleles have been reported, *lks5.h* (*lk*, *f*) in two-rowed Glacier (3); and a mutant in Morex (Clho 15773) (12); *lks5.p* in G7118 (leafy lemma, GSHO 1780) mutant stock (1, 3, 4, 11).

Mutant used for description and seed stocks:

lks5.f in Clho 5641 (GSHO 1297); *ari-c.2* in Bonus (NDB 115847, GSHO 1651); *lks5.f* in Bowman (PI 483237)*6 (GSHO 2014), in Bowman*7 (BW493, NGB 20721); *ari-c.2* in Bowman*7 (GSHO 2013, BW040, NGB 20448); *lks5.p* from G7118 in Bowman*4 with *lel1.a* (BW474, NGB 20704); *lks5.p* from G7118 in Bowman*5 (BW475, NGB 20705).

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Prepared:

T.E. Haus. 1978. *Barley Genet. Newsl.* 8:156.

Revised:

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 J.D. Franckowiak and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:197.
 J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:110-111.

BGS 182, Extra floret-a, *flo-a*

Stock number: BGS 182
Locus name: Extra floret-a
Locus symbol: *flo-a*

Previous nomenclature and gene symbolization:
None.

Inheritance:

Monofactorial recessive (3, 4).

Location in chromosome 6H (1); *flo-a.1* is associated with SNP markers 1_0539 to 1_0040 (positions 76.05 to 107.26 cM) in 6H bins 06 to 07 of the Bowman backcross-derived line BW367 (1); *flo-a.3* is associated with SNP markers 2_0746 to 1_1246 (positions 125.86 to 134.55 cM) in 6H bin 08 of the Bowman backcross-derived line BW368 (1); *flo-a.5* is associated with SNP markers 1_0061 to 1_1246 (positions 70.15 to 134.55 cM) in 6H bins 05 to 08 of the Bowman backcross-derived line BW369 (1), likely in 6H bin 07.

Description:

Extra bracts develop occasionally at the base of the central spikelet on the abaxial side. Formation of the extra bracts is most common in the central portion of the spike, but rarely will the bracts form another spikelet (2, 4). Except of the occasional development of a bract below the central spikelet, the Bowman backcross-derived lines for mutants at the *flo-a* locus, BW367, BW368, and BW369 were similar to Bowman (2).

Origin of mutant:

An ethylene imine induced mutant in Foma (Clho 11333) (4).

Mutational events:

flo-a.1 (NGB 114271, GSHO 1741) in Foma, *flo-a.3* (NGB 114273, GSHO 1742, previously named *flo-b.3*) in Foma; *flo-a.5* (NGB 114275, GSHO 1743, previously named *flo-c.5*) in Foma (4).

Mutant used for description and seed stocks:

flo-a.1 in Foma (GSHO 1741, NGB 114271); *flo-a.3* in Foma (GSHO 1742, NGB 114273); *flo-a.5* in Foma (GSHO 1743, NGB 114275); *flo-a.1* in Bowman (PI 483237)*5 (GSHO 2005), in Bowman*7 (BW367, NGB 20606); *flo-a.3* in Bowman (PI 483237)*6 (GSHO 2128, BW368, NGB 20607); *flo-a.5* in Bowman (PI 483237)*7 (GSHO 1877, BW369, NGB 20608).

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Prepared:

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Revised:

J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:112.

BGS 201, Chlorina seedling 7, *fch7*

Stock number: BGS 201
Locus name: Chlorina seedling 7
Locus symbol: *fch7*

Previous nomenclature and gene symbolization:

Chlorina seedling 7 = *f7* (3).
Chlorina seedling 7 = *clo-f7^{f7}* (4).

Inheritance:

Monofactorial recessive (3).
Located in chromosome 1HL (3); about 4.7 cM proximal from the *trd1* (third outer glume 1) locus and about 22.7 cM distal from the *Blp1* (black lemma and pericarp 1) locus (3); *fch7.h* is associated with SNP markers 1_0911 to 1_1481 (positions 177.51 to 186.13 cM) in 1H bin 13 of Bowman backcross-derived line BW363 (1); likely in 1H bin 13.

Description:

Seedlings are light green and remain light green until near maturity (3). Plant vigor and seed yields are reduced, and developmental stages are delayed. Heading of plants in the Bowman backcross-derived line BW363 was delayed by up to 9 days compared to Bowman, but plant height was normal in most environments. Kernel weights were reduced by about 10% and grain yields were 85 to 95% of normal (2).

Origin of mutant:

A spontaneous mutant in Smyrna (3).

Mutational events:

fch7.h in Smyrna (Smyrna II, GSHO 4) (3); *fch7.i* in Smyrna (Smyrna III) (5).

Mutant used for description and seed stocks:

fch7.h in Smyrna (GSHO 4); *fch7.h* in Bowman (PI 483237)*7 (GSHO 2058, BW363, NGB 20602).

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Prepared:

T.E. Haus and T. Tsuchiya. 1971. *Barley Genet. Newsl.* 1:146.

Revised:

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J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:206.
J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:113.

BGS 208, Fragile stem 2, *fst2*

Stock number: BGS 208
Locus name: Fragile stem 2
Locus symbol: *fst2*

Previous nomenclature and gene symbolization:

Fragile stem 2 = *fs2* (13).

Hordeum vulgare Cellulose synthase gene 1 = *HvCesA4* (1).

Inheritance:

Monofactorial recessive (10, 13).

Located in chromosome 1HL (9, 11, 12); over 19.0 cM proximal from the *nec1* (necrotic leaf spot 1) locus (4); 1.9 cM distal from molecular markers *wg789d* and *bcd351b* in 1H bin 08 (1); *fst2.b* is associated with SNP markers 1_0259 to 2_0997 (positions 70.78 to 89.01 cM) in 1H bins 07 to 08 of the Bowman backcross-derived line BW374 (1), in 1H bin 08.

Description:

The brittle leaf and stem characteristics of *fst2* plants are similar to those of *fst1* plants (9). Leaves and stems are very fragile and easily broken when slightly bent (13). Young leaves generally wither in the afternoon in the greenhouse and in the field during the spring. Most of the leaf blade tips turn yellow prior to heading and gradual die back is observed (9). Plants are about one-half normal height when protected in the greenhouse, but in the field plants are weak and are easily damaged by wind. Culm internodes are often curved (3). For the semidwarf, brittle stem mutants, *fst2* alleles *fst2.b* and *fst2.e* in their original stocks, the maximum flexural load (Newtons) required to bend the midpoint of each internode was 2 to 3 times lower than the load causing bending in their parents (1, 7, 8). Heading was delayed about four days in the Bowman backcross-derived line BW374. Compared to Bowman, plants of the BW374 line were about 1/2 normal height. Spikes had 3 to 4 fewer kernels. Kernels were small and thin and 1/2 to 2/3 of normal weight. Grain yields are very low (3). The *fst2* mutants were shown to have reduced levels of crystalline cellulose in their culms compared with their parental lines (6, 8). A custom-designed microarray used by Burton et al. (1) revealed a marked decrease in transcript levels of mRNA for the *HvCesA4* cellulose synthase gene. Sequencing of the *HvCesA4* gene of *fst2* mutants revealed the presence of a 964-bp solo long terminal repeat of a Copia-like retroelement in the first intron, which interferes with transcription or processing of the mRNA from the of the *HvCesA4* gene (1).

Origin of mutant:

A spontaneous mutant in Oshichi (OUJ755, PI 190273) (9, 10, 13).

Mutational events:

fst2.b (OUX054) in Oshichi (Oshichi-hen, OUL006, GSHO 578) (9, 10, 13); *fst2.e* (OUM245) In Shiroseto (OUJ156) (8).

Mutant used for description and seed stocks:

fst2.b in Oshichi (GSHO 578, OUX054); *fst2.b* in Bowman (PI 483237)*7 (GSHO 2046), *fst2.b* in Bowman*8 (BW374, NGB 20613).

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Revised:

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BGS 214, Early maturity 8, *eam8*

Stock number: BGS 214
Locus name: Early maturity 8
Locus symbol: *eam8*

Previous nomenclature and gene symbolization:

Early heading k = *ea_k* (27).
Early maturity-a = *ea-a* (9, 22).
Praematurum-a = *mat-a* (4, 9, 14, 15, 27).
Erectoides-o = *ert-o* (9, 19).
Hordeum vulgare Early flowering 3 = *HvElf3* (28).

Inheritance:

Monofactorial recessive (4, 8).
Located in chromosome 1HL (22), about 11.4 cM distal from the *trd1* (third outer glume 1) locus and 20.9 cM distal from the *Blp1* (black lemma and pericarp 1) locus (22, 25); associated with SNP markers 2_0603 to 2_0138 (positions 199.04 to 202.26 cM) in 1H of the Bowman backcross-derived line BW290 (3); associated with SNP markers 1_0782 to 1_0443 (positions 193.83 to 206.12) in 1H of the Bowman backcross-derived line BW289 (3); associated with SNP markers 1_0911 to 1_1509 (positions 177.51 199.04) in 1H of the Bowman backcross-derived line BW319 (3), in 1H bin 14.

Description:

Early heading is associated with decreased culm length, spike length, kernels per spike, and grain yield (17, 25, 27). Mutant plants are day-length neutral or photoperiod insensitive when grown in the fall at Kurashiki, Japan (27). They head about 20 days earlier than the standard mid-season cultivar, Akashinriki. Day-length neutrality was observed in early heading mutants isolated from spring barley in Sweden (2, 10). Under controlled environmental conditions, number of days to heading did not change as photoperiod is altered (2, 11). All *mat-a* induced mutants were characterized by yellowish-green seedlings at an early stage of development under controlled environmental conditions (1). Other *eam8* mutants showed a similar response by becoming yellow green under specific growing conditions, 8 to 12 hours of illumination at low temperatures (below 10°C) plus high temperature (20°C or higher) during the dark period (6, 22, 25). The color change is caused by photothermal stress, which increases the zeaxanthin content at the expense of chlorophyll and other pigments (6, 20, 25). The mutant stock *mat-a.8* was released as the cultivar Mari (10, 12). When grown under 12 h days, the levels of phytochrome B (*phyB*) decreased in light-grown BMDR-1 plants, containing a mutant allele at the *eam8* locus, compared to normal plants (13). The instability of *phyB* content was reported to be responsible for photoperiod insensitivity of *eam8* mutants (13). Under continuous light and with far-red light treatment for seven days, most differences in heading date between BMDR-1 and BMDR-8 (Shabet) are eliminated (20). The *Mat-a* or *Eam8* (*HvElf3*) locus has been cloned and is a homolog of the *Arabidopsis thaliana* circadian clock regulator Early Flowering 3 (*Elf3*). Among 87 *mat-a* alleles identified >20 different *mat-a* alleles had mutations leading to the defective putative ELF3 protein (28). The effects *mat-a* mutants on the development of reproductive structures might be explained by pronounced expression of flowering inducing genes like *Gigantea* (*AtGI*) (28).

Origin of mutant:

An X-ray induced mutant in Maja (PI 184884, NGB 8815) (7, 8, 11); natural occurrence in Kinai 5 (OUJ493) and Kagoshima Gold (OUJ219) (22, 26).

Mutational events:

ert-o.16 (NGB 112618, GSHO 489) in Maja (7); *eam8.k* in Kagoshima Gold (OUJ 219), Kinai 5 (OUJ493, GSHO 765, Clho 11560), and Kindoku (OUU332) (22, 23, 26); *mat-a.8* (NGB 1491, NGB 4694, NGB 14656, NGB 110008), *-a.11* (NGB 110011), *-a.12* (NGB 110012) in Bonus (PI 189763) (8, 15); *mat-a.27* (NGB 110027), *-a.45* (NGB 110045), *-a.46* (NGB 110046), *-a.48* (NGB 110048), *-a.62* (NGB 110062) in Bonus, *-a.110* (NGB 110110), *-a.130* (NGB 110130), *-a.153* (NGB 110153), *-a.221* (NGB 110221), *-a.238* (NGB 110238), *-a.255* (NGB 110255), *-a.272* (NGB 110272), *-a.274* (NGB 110274), *-a.287* (NGB 110287), *-a.289* (NGB 110289), *-a.294* (NGB 110294), *-a.325* (NGB 110325), *-a.338* (NGB 110338), *-a.370* (NGB 110370), *-a.384* (NGB 110384), *-a.390* (NGB 110390), *-a.404* (NGB 110404), *-a.406* (NGB 110406), *-a.407* (NGB 110407) in Foma (Clho 11333), *-a.509* (NGB 110509), *-a.641* (NGB 110641), *-a.703* (NGB 110703), *-a.733* (NGB 110733), in Kristina (NGB 1500), *-a.753* (NGB 110753), *-a.796* (NGB 110796), *-a.797* (NGB 110797), *-a.813* (NGB 110813), *-a.832* (NGB 110832), *-a.903* (NGB 116858), *-a.909* (NGB 117440), *-a.921* (NGB 117452) in Bonus, *-a.961* (NGB 117492), *-a.970* (NGB 117501), *-a.976* (NGB 117507), *-a.984* (NGB 117515), *-a.1011* (NGB 117542), in Sv 79353, *-a.1032* (NGB 117563), *-a.1033* (NGB 117564), *-a.1034* (NGB 117565), *-a.1035* (NGB 117566), *-a.1036* (NGB 117567), *-a.1037* (NGB 117568), *-a.1039* (NGB 117570), *-a.1040* (NGB 117571), *-a.1041* (NGB 117572), *-a.1042* (NGB 117573), *-a.1043* (NGB 117574), *-a.1044* (NGB 117575), *-a.1045* (NGB 117576), *-a.1046* (NGB 117577), *-a.1047* (NGB 117578), *-a.1048* (NGB 117579), *-a.1049* (NGB 117580) in Sv Vg74233 (14); *mat-a.1050* (NGB 117581), *-a.1051* (NGB 117582), *-a.1052* (NGB 117583), *-a.1053* (NGB 117584), *-a.1054* (NGB 117585), *-a.1055* (NGB 117586), *-a.1056* (NGB 117587), *-a.1057* (NGB 117588), *-a.1058* (NGB 117589), *-a.1059* (NGB 117590), *-a.1060* (NGB 117591), *-a.1061* (NGB 117592), *-a.1062* (NGB 117593), *-a.1063* (NGB 117594), *-a.1064* (NGB 117595), *-a.1065* (NGB 117596), *-a.1067* (NGB 117598), *-a.1069* (NGB 117600), *-a.1070* (NGB 117601), *-a.1071* (NGB 117602), *-a.1072* (NGB 117603), *-a.1073* (NGB 117604), *-a.1074* (NGB 117605) in Sv Vg74233 (16); *eam8.q* (Ea8), *eam8.r* (Ea9), *eam8.s* (Ea10), *eam8.t* (Ea16) in Chikurin Ibaraki 1 (OUJ069, Clho 7370, GSHO 783) (24); *eam8.u* (Mut 2571) in Donaria (PI 161974) (6, 18); *eam8.v* in Munsing (Clho 6009, GSHO 636) (5, 20, 21); *eam8.w* in Early Russian (Clho 13839) (5), BMDR-1 (*eam8.y*) from the original mutant in a dwarf line backcrossed to Shabet (Clho 13827) (20).

Mutant used for description and seed stocks:

eam8.k in Kinai 5 (OUJ266, GSHO 765, Clho 11560); *ert-o.16* in Maja (GSHO 489, NGB 112618); *eam8.k* in Bonus*5 (26); *mat-a.8* in Tochigi Golden*5 (26); *eam8.u* in Munsing/7*Titan (Clho 16526) (21); *eam8.k* in Bowman (PI 483237)*7 (GSHO 2063, BW289, NGB 20573); *eam8.w* in Bowman*7 (BW290, NGB 20574); *ert-o.16* in Bowman*7 (GSHO 2064), in Bowman*8 (BW319, NGB 22114).

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Revised:

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BGS 231, Curly 5, *cur5*

Stock number: BGS 231
Locus name: Curly 5
Locus symbol: *cur5*

Previous nomenclature and gene symbolization:

Curly 5 = *cu5* (3).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 2HS (1); *cur5.h* is associated with SNP markers 1_1078 to 2_0476 (positions 66.78 to 96.47 cM) in 2HL bins 05 to 07 of the Bowman backcross-derived line BW225 (1); *cur5.h* is associated with SNP markers 1_0498 to 2_0476 (positions 81.43 to 96.47 cM) in 2HL bin 07 of the Bowman backcross-derived line BW250, which also contains dusky 1 (*dsk1.a*) (1). Previously located in chromosome 1HS (4); based on linkage drag with the *sls1* (small lateral spikelet 1) locus (5).

Description:

Leaves are short and partially coiled, and awns are slightly coiled. Plants are semidwarf (2/3 normal height), have relatively short spikes, and are relatively weak (2, 3). Plants of the Bowman backcross-derived line for *cur5.h*, BW225, headed 3 days later than Bowman and were about half as tall. Leaf blades of BW225 were short and narrow compared to those of Bowman. Spikes contain 5 fewer kernels, kernel were narrower (3.3 vs. 3.7 mm), and kernel weights were 10 to 15% lower (3).

Origin of mutant:

A sodium azide induced mutant in Glenn (Clho 15769) (2).

Mutational events:

cur5.h (GSHO 1710) in Glenn (2, 3).

Mutant used for description and seed stocks:

cur5.h in Glenn (GSHO 1710); *cur5.h* in Bowman (PI 483237)*8 (BW225, NGB 22052); *cur5.h* with *dsk1.a* in Bowman*7 (GSHO 2045, BW250, NGB 22075).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
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3. Franckowiak, J.D. (Unpublished).
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Prepared:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:229.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:120.

BGS 244, Dense spike 11, *dsp11*

Stock number: BGS 244
Locus name: Dense spike 11
Locus symbol: *dsp11*

Previous nomenclature and gene symbolization:

Dense spike am = *dsp.am* (2).
Dense spike an = *dsp.an* (2).
Dense spike ao = *dsp.ao* (2).

Inheritance:

Monofactorial incomplete dominant (2).
Located in chromosome 1HL (1); *dsp11.am* is associated with SNP markers 2_0798 to 1_0798 (positions 82.35 to 90.92 cM) in 1H bin 08 of the Bowman backcross-derived line BW260 (1); *dsp11.ao* is associated with SNP markers 2_1000 to 2_0956 (positions 76.28 to 98.23 cM) in 1H bins 08 to 09 of the Bowman backcross-derived line BW262 (1); *dsp11.an* is associated with SNP markers 1_0259 to 1_0466 (positions 70.78 to 119.29 cM) in 1H bins 07 to 10 of the Bowman backcross-derived line BW261 (1), likely in 1H bin 08.

Description:

All three Bowman backcross-derived lines with short rachis internodes from crosses to Akashinriki retained an overlapping region in 1HL. The line BW260 with *dsp11.am* was used for trait comparisons because other two lines also retained SNP markers on other chromosomes (1). In comparison to Bowman, plants of Bowman backcross-derived line BW260 were slightly shorter and had more compact spikes, rachis internode lengths 3.5 vs. 4.6 mm. Kernels were shorter, 8.6 vs. 9.7 mm, and about 10% lighter. Test weights were slightly lower and grain yields were about 3/4 those for Bowman. The other two Bowman backcross-derived lines in which the *dsp11* segment was retained, BW261 (*dsp11.an*) and BW262 (*dsp11.ao*) plants had slightly shorter rachis internodes and kernels than Bowman. Kernels were about 30% lighter and yields were lower. BW261 plants were slightly taller than Bowman plants while BW262 was shorter (2). A common chromosome segment of 6HL was retained in both BW261 and BW262, with the SNP markers overlapping in the region from 1_0645 to 1_1187 (positions 190.38 to 195.01 cM) in 6H bin 11 (1).

Origin of mutant:

Natural occurrence in Akashinriki (OUJ659, PI 467400) (2), extracted from an ethyl methanesulfonate induced mutant (OUM070) of Akashinriki (3, 4).

Mutational events:

dsp11.am (OUM070, GSHO 1722) in Akashinriki, *dsp11.an* (OUM105) in Akashinriki, *dsp11.ao* (OUM125, GSHO 1723) in Akashinriki (4).

Mutant used for description and seed stocks:

dsp11.am (OUM70, GSHO 1722) in Akashinriki; *dsp11.am* in Bowman (PI 483237)*4 (GSHO 2244), in Bowman*6 (BW260, NGB 22085); *dsp11.an* from Akashinriki in Bowman *4 (BW261, NGB 22086); *dsp11.ao* from Akashinriki in Bowman*6 (GSHO 2039), *dsp11.ao* in Bowman*8 (BW262, NGB 22087).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).

3. Konishi, T. 1970. Studies on EMS-induced mutation in barley III. Nogaku Kenkyu 53:141-152.

4. Konishi, T. 1975. Characteristics and inheritance of EMS-induced mutants in barley. Nogaku Kenkyu 55:53-56.

Prepared:

J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:121-122.

BGS 252, Early maturity 7, *eam7*

Stock number: BGS 252
Locus name: Early maturity 7
Locus symbol: *eam7*

Previous nomenclature and gene symbolization:

Early heading = *ec* (9).
Early maturity 7 = *ea7* (8).

Inheritance:

Monofactorial recessive (4, 9).
Located in chromosome 6HS (9); about 0.5 cM from the *rob1* (orange lemma 1) locus (8); about 3.0 cM from the centromere (6); *eam7.g* is associated with SNP markers 2_0886 to 1_0978 (positions 3.28 to 156.09 cM) in 6H bins 01 to 09 of the Bowman backcross-derived line BW288 (1); *eam7.g* is associated with homozygous SNP markers 2_0882 to 1_0615 (positions 6.19 to 28.27 cM) in 6H bins 01 to 02 of the Bowman backcross-derived line BW287 (1), likely in 6H bin 02.

Description:

Under short-day conditions in California, USA, mutant plants bloom about 4 weeks before California Mariout, produced relatively few tillers, were fine stemmed, and were relatively short. Differences were less pronounced under long-day conditions (8). Mutants were partially insensitive to photoperiod and have a vernalization requirement (9). Under long-day conditions, segregates expressing the *eam7.g* gene were difficult to identify (7). When the *Eam1.a* (early maturity 1) gene is not present, *eam7.g* plants headed 10 to 14 days earlier than Bowman in nurseries at Yuma, Arizona, USA, but only 3 to 5 days earlier at Fargo, North Dakota, USA. (2) The *Eam1.a* gene present in California Mariout apparently interacts with the *eam7.g* allele under short-day conditions to cause extreme earliness (2). The Bowman backcross lines for *eam7.g*, BW287 and 288, were 4 to 10 days earlier than Bowman under short days, but no differences were observed under long days (2). The *HvCO7* (*Hordeum vulgare* *CONSTANS 7*) gene was located on the same chromosome arm as *eam7* gene (5).

Origin of mutant:

A spontaneous mutant in Atlas (PI 539108) identified as Atsel (CIho 6250) (4); present in male sterile Club Mariout/6*California Mariout (PI 527380) (3, 9).

Mutational events:

eam7.g in BC₆ California Mariout (GBC326, GSHO 579) (4, 8); *eam7.n* (Ea1), *eam7.o* (Ea2), *eam7.p* (Ea3) in Chikurin Ibaraki 1 (OUJ069, CIho 7370) (10).

Mutant used for description and seed stocks:

eam7.g in BC₆ California Mariout (GSHO 579); *eam7.g* in Bowman (PI 483237)*3 (GSHO 2068, BW288, NGB 20572), *eam7.g* in Bowman*2 (BW287, NGB 20571).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Gallagher, L.W. (Unpublished).
4. Gallagher, L.W., K.M. Soliman, and H. Vivar. 1991. Interactions among loci conferring photoperiod insensitivity for heading time in spring barley. *Crop Sci.* 31:256-261.
5. Griffiths, S. R.P. Dunford, G. Coupland, and D. A. Laurie. 2003. The evolution of *CONSTANS*-like gene families in barley, rice, and Arabidopsis. *Plant Physiol.* 131:1855-1867.

6. Kasha, K.G., D.E. Falk, and A. Ho-Tsai. 1978. Linkage data with genes on chromosome 6. *Barley Genet. Newsl.* 8:61-65.
7. Kramer, H.H., and B.A. Swomley Blander. 1961. Orienting linkage maps on the chromosomes of barley. *Crop Sci.* 1:339-342.
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9. Ramage, R.T., and C.A. Suneson. 1958. A gene marker for the g chromosome of barley. *Agron. J.* 50:114.
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Prepared:

C.R. Burnham. 1971. *Barley Genet. Newsl.* 1:155. Early heading, *ea7*.

Revised:

J.D. Franckowiak and L.W. Gallagher. 1997. *Barley Genet. Newsl.* 26:233.

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:123-124.

BGS 263, Curly 3, *cur3*

Stock number: BGS 263
Locus name: Curly 3
Locus symbol: *cur3*

Previous nomenclature and gene symbolization:

Curly 3 = *cu3* (5).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 6HL (5); about 22.9 cM distal from the *cul2* (uniculm 2) locus (4, 5); *cur3.e* is associated with SNP markers 2_0488 to 1_1147 (positions 119.40 to 137.78 cM) in 6H bins 07 to 08 of the Bowman backcross-derived line BW222 (1), likely in 6H bin 08.

Description:

Stem internodes are curved in a bow-like manner and awns are slightly coiled (5).

Seedlings elongate rapidly and leaves are nearly twice as long as normal. Seedlings homozygous for the *cur3.e* allele do not show additional elongation in response to gibberellic acid treatment (3). Plants of the Bowman backcross-derived line for *cur3.e*, BW222, had an open crown semi-prostrate early growth and were about 15% shorter than Bowman. Kernels of BW222 were slightly small and weighed 5 to 10% less. The grain yields of BW222 were about 3/4 those of Bowman (2).

Origin of mutant:

An X-ray induced mutant in Akashinriki (OUJ659, PI 467400) isolated by A. Yamashita (5).

Mutational events:

cur3.e (OUM301, GSHO 1707) in Akashinriki (4, 5).

Mutant used for description and seed stocks:

cur3.e in Akashinriki (GSHO 1707, OUM301); *cur3.e* in Bowman (PI 483237)*6 (GSHO 2087), in Bowman*7 (BW222, NGB 22049).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes: A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
4. Hayashi, J., T. Konishi, I. Moriya, and R. Takahashi. 1984. Inheritance and linkage studies in barley VI. Ten mutant genes located on chromosomes 1 to 7, except 3. *Ber. Ohara Inst. landw. Biol., Okayama Univ.* 18:227-250.
5. Hayashi, J., R. Takahashi, I. Moriya, and T. Nobuoka. 1978. Linkage studies of two mutant genes on chromosomes 1 and 6. *Barley Genet. Newsl.* 8:48-50.

Prepared:

J.D. Franckowiak and T. Konishi. 1997. *Barley Genet. Newsl.* 26:243.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:125.

BGS 264, Mottled leaf 5, *mtt5*

Stock number: BGS 264
Locus name: Mottled leaf 5
Locus symbol: *mtt5*

Previous nomenclature and gene symbolization:

Mottled f = *mt*, *f* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 6HL (3); about 6.4 cM distal from the *rob1* (orange lemma 1) locus (3); *mtt5.f* is associated with SNP markers 2_0936 to 2_0577 (positions 71.39 to 117.10 cM) in 6H bins 06 to 07 of the Bowman backcrossed-derived line BW603 (1), likely in 6H bin 07.

Description:

Mottled bands occur on the leaf blade and sheath and are retained until heading (3). The first few seedling leaves often do not show the mottled trait. Plants of Bowman backcross-derived line for *mtt5.f*, BW603, were less vigorous than Bowman and heading was slightly delayed. BW603 had slightly lower kernel weights and grain yields ranging from 1/2 to 3/4 those of Bowman (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (3).

Mutational events:

mtt5.f (OUM022, GSHO 2410) in Akashinriki (3).

Mutant used for description and seed stocks:

mtt5.f in Akashinriki (GSHO 2410, OUM022); *mtt5.f* in Bowman (PI 483237)*6 (GSHO 2084), in Bowman*7 (BW603, NGB 22169).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
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Prepared:

T. Konishi and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:244.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:126.

BGS 302, Mottled leaf 2, *mtt2*

Stock number: BGS 302
Locus name: Mottled leaf 2
Locus symbol: *mtt2*

Previous nomenclature and gene symbolization:

Mottled leaf 2 = *mt2* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 5HL (3); about 26.1 cM proximal from the *srh1* (short rachilla hair 1) locus (3); *mtt2.b* is associated with SNP markers 2_0645 to 2_0850 (positions 134.85 to 157.13 cM) in 5H bins 08 to 09 of the Bowman backcross-derived line BW601 (1), likely in 5H bin 08.

Description:

Yellow to ivory bands, rarely necrotic, appear at emergence on the seedling leaf. They gradually disappear and are absent at heading (3). Expression is better when alternating temperatures occur, but even under constant temperatures, the tip of the first leaf is yellow or pale green (2). The Bowman backcross-derived line for the *mtt2.b* mutant, BW601, was agronomically and morphologically similar to Bowman (2).

Origin of mutant:

A Rad-Beryll induced mutant in Montcalm (Clho 7149) (3).

Mutational events:

mtt2.b (GSHO 1398, Alb Acc 285) in Montcalm (3).

Mutant used for description and seed stocks:

mtt2.b in Montcalm (GSHO 1398); *mtt2.b* in Bowman*7 (GSHO 2099, BW601, NGB 22167).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
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Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:161.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:253.

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:127.

BGS 322, Dusky 1, *dsk1*

Stock number: BGS 322
Locus name: Dusky 1
Locus symbol: *dsk1*

Previous nomenclature and gene symbolization:
None.

Inheritance:

Monofactorial recessive (5).

Located in chromosome 5HL (5), about 17.6 cM distal from the *srh1* (short rachilla hair 1) locus and 7.8 cM proximal from the *raw1* (smooth awn 1) locus (3, 4); *dsk1.a* is associated with SNP markers 1_0024 to 2_1273 (positions 165.44 to 171.34 cM) in 5H of the Bowman backcrossed-derived lines BW250 and BW251 (1), in 5H bin 10.

Description:

After heading as the plant matures, leaf blades begin to dehydrate and turn a dusky, olive-gray color. Many, small dark spots occur scattered over the surface of the olive-gray plant parts. Even after maturity, spikes and culms remain faint green in color (5). When plants of the Bowman backcross-derived for *dsk1.a*, BW251 are grown in the greenhouse, moisture stress causes lower leaves to die rapidly without loss of green pigments. Anthers are pale green instead of yellow at anthesis. Other plant characteristics of BW251 appear in the normal range compared with those of Bowman (2).

Origin of mutant:

A gamma-ray induced mutant in Chikurin Ibaraki 1 (OUJ069, CIho 7370) isolated by A. Yamashita (5).

Mutational events:

dsk1.a in Chikurin Ibaragi 1 (OUM299, GSHO 1714) (4, 5).

Mutant used for description and seed stocks:

dsk1.a in Chikurin Ibaragi 1 (GSHO 1714); *dsk1.a* with *cur5.h* in Bowman (PI 483237, BW250, NGB 22075)*7 (GSHO 2120), in Bowman*8 (BW251, NGB 22076).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiology* 155:617-627.
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Prepared:

J.D. Franckowiak and T. Konishi. 1997. *Barley Genet. Newsl.* 26:270.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:128.

BGS 325, Curly lateral 1, *cr1*

Stock number: BGS 325
Locus name: Curly lateral 1
Locus symbol: *cr1*

Previous nomenclature and gene symbolization:

Curly laterals = *cu* (5).

Curly laterals = *cl* (4).

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 6H (1); *cr1.a* is associated with SNP markers 2_1473 to 2_1256 (positions 87.67 to 118.33 cM) in 6H bins 06 to 07 of the Bowman backcross-derived line BW194 (1). Previously reported to be in 5HL over 30.4 cM distal from the *raw1* (smooth awn 1) locus (4, 5); linkage to the *Rph9* (reaction to *Puccinia hordei* 9) locus was not found (3).

Description:

Awns on lateral spikelets are curly or wavy, and lateral spikelets may be malformed and partially sterile. Central spikelets may have a twisted awn occasionally (4). The curly lateral trait is not expressed in all tillers (4). The *cr1.a* gene is expressed better in six-rowed spikes. In the Bowman backcross-derived line for *cr1.a*, BW194, awns seemed thinner and the awns of some spikelets were bent at odd angles (2). The awns of BW194 were about 20% shorter than those of Bowman. Kernels were about 10% shorter and thinner, and their weights were about 10% less than those of Bowman. Heading was often delayed by one or two days and spikes had 2 to 3 fewer kernels. Grain yields of BW194 were 1/2 to 2/3 those of Bowman (2).

Origin of mutant:

A gamma-ray induced mutant in Montcalm (Clho 7149) (4).

Mutational events:

cr1.a in Montcalm (Alb Acc 305, GSHO 1211) (4).

Mutant used for description and seed stocks:

cr1.a in Montcalm (GSHO 1211); *cr1.a* in Bowman (PI 483237)*3 (GSHO 2146), in Bowman*6 (BW194, NGB 22026).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
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Prepared:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:273.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:129.

BGS 326, Broad leaf 1, *blf1*

Stock number: BGS 326
Locus name: Broad leaf 1
Locus symbol: *blf1*

Previous nomenclature and gene symbolization:

Bredbladig = *bb* (5).
Latifolium (3).
Broad leaf = *bb* (4).

Inheritance:

Monofactorial recessive (3, 5).
Located in chromosome 2HL (1); *blf1.a* is associated with SNP markers 1_0525 to 2_1078 (positions 65.03 to 118.78 cM) in 2H bins 07 to 08 of the Bowman backcross-derived line BW058 (SNP associations on 2HL and 6HL are shorter) (1). Previously reported to be in 5HL about 20.6 cM proximal from the *srh1* (short rachilla hair 1) locus (5).

Description:

Plants are somewhat lighter green than normal. All leaf blades are very broad, about twice normal width, and markedly crinkled, especially at the margins (5). Leaf blades of flag minus 1 leaves of the Bowman backcross-derived line BW058 are nearly twice as wide as those of Bowman. Heading of BW058 is delayed by 5 to 10 days compared to Bowman; plants are slightly shorter; and kernel size and grain yield are slightly less (2).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (5).

Mutational events:

blf1.a in Bonus (Alb Acc 55, GSHO 1393) (5).

Mutant used for description and seed stocks:

blf1.a in Bonus (GSHO 1393); *blf1.a* in Bowman (PI 483237)*1 (GSHO 2166), in Bowman*3 (BW058, NGB 20466).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiology* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
4. Robertson, D.W., G.A. Wiebe, R.G. Shands, and A. Hagberg. 1965. A summary of linkage studies in cultivated barley, *Hordeum* species: Supplement III, 1954-1963. *Crop Sci.* 5:33-43.
5. Walker, G.W.R., J. Dietrich, R. Miller, and K.J. Kasha. 1963. Recent barley mutants and their linkages II. Genetic data for further mutants. *Can. J. Genet. Cytol.* 5:200-219.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:274.

Revised:

J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:130.

BGS 328, Breviaristatum-e, *ari-e*

Stock number: BGS 328
Locus name: Breviaristatum-e
Locus symbol: *ari-e*

Previous nomenclature and gene symbolization:

Breviaristatum-1 = *ari-1* (6, 7).
Short awn 9 = *lk9* (18).
Golden Promise erectoides = *GPert* (17).

Inheritance:

Monofactorial recessive (6).
Located in chromosome 5HL (11, 12, 13, 17); about 5.6 cM proximal from the *cer-zj* (*eceriferum-zj*) locus (15, 16); near SSR molecular marker Bmag337 (3); *ari-e.GP* is close to SNP marker 2_1239 (9); *ari-e.1* is associated with SNP markers 2_1480 and 3_0285 (position 137.96 cM) in 5H bin 08 of the Bowman backcross-derived line BW042 (1); *ari-e.GP* is associated with SNP markers 1_1198 to 2_0449 (positions 73.70 to 154.37 cM) in 5H bins 02 to 09 of the Bowman backcross-derived line BW043 (1), in 5H bin 06.

Description:

Awns are about 2/3 normal length, plants are 3/4 to 5/6 normal height, and kernels are smaller (7, 17). Awns and spikes are more erect than those of normal sibs (8). Mutant alleles at the *ari-e* locus are associated with salt tolerance, lower accumulation of Na⁺ (2, 3, 10), and show relative insensitivity to GA₃ (10). The *ari-e.GP* mutant is described as an elongation (*elo*) type of semidwarf mutant based on cell size reduction in leaf blades (2). Plants of the Bowman backcross-derived lines for *ari-e.1* (BW042) and *ari-e.GP* (BW043) are about 3/4 as tall as Bowman and have awns that are about half as long. Rachis internodes and leaf blades are slightly shorter. Kernels of BW042 and BW043 are about 10% shorter than those of Bowman and weighed about 10% less. Grain yields of BW042 and BW043 were often less than those of Bowman (5).

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763) (7).

Mutational events:

ari-e.1 in Bonus (NGB 115846, GSHO 1653) (7); *ari-e.30* (NGB 115879), *-e.39* (NGB 115889) in Bonus (8); *ari-e.119* (NGB 115931), *-e.156* (NGB 115966) in Foma (Clho 11333) (7); *ari-e.166* (NGB 11976), *-e.178* (NGB 115988), *-e.222* (NGB 116301) in Foma (8); *ari-e.228* (NGB 116038) in Foma (7); *ari-e.GP* (Golden Promise, PI 343079, GSHO 1733) in Maythorpe (PI 260893) (3, 4, 14), but PI 260893 has three genomic regions that differ from Golden Promise (19).

Mutant used for description and seed stocks:

ari-e.1 in Bonus (GSHO 1653); *ari-e.GP* in Maythorpe (GSHO 1733); *ari-e.1* in Bowman (PI 483237)*7 (GSHO 2104, BW042, NGB 20450); *ari-e.GP* in Bowman*7 (GSHO 2105, BW043, NGB 20451).

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:276.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:131-132.

BGS 330, Erectoides-g, *ert-g*

Stock number: BGS 330
Locus name: Erectoides-g
Locus symbol: *ert-g*

Previous nomenclature and gene symbolization:

Erectoides-24 = *ert-24* (3).

Brachytic 3 = *br3* (12).

Inheritance:

Monofactorial recessive (3, 7).

Located in chromosome 1HL (1); *ert-g.24* is associated with retained SNP markers 1_1359 to 2_1413 (positions 81.62 to 95.80 cM) in 1H bins 08 and 09 of the Bowman backcross-derived line BW309, but only SNP markers 1_1359 to 1_1256 (positions 81.62 to 82.35 cM) in 1HL match the Bonus haplotype (1), likely in 1H bin 08. Previously located in chromosome 5HL (4, 5, 6, 7); about 4.7 cM proximal from the *cer-i* (*eceriferum-i*) locus (8, 9); about 3.1 cM distal from the *lax-a* (*laxatum-a*) locus (7, 10).

Description:

Compact spikes are caused by reduced rachis internode length, with values from 2.1 to 2.4 mm (7). Awns and lateral spikelets are closely pressed to the spike, the upper part of the straw is spirally twisted, anthers are short and thick, and the ligule is small. Spikes tend to have a whitish color at maturity caused by a dense surface wax covering (7). GA₃ treatment of plants as the flag leaf emerges decreases spike density (11). Plants have a brachytic-like appearance (12) and showed slightly reduced seed set. Plants of the Bowman backcross-derived line with *ert-g.24*, BW309, were slightly shorter than Bowman and rachis internode lengths were 3.3 vs. 4.5 mm. Kernels were slightly shorter and wider than those of Bowman. Kernels weights and grain yields of BW309 tended to be slightly lower (2). Allelism tests are needed to confirm that BW309 contains the *ert-g.24* mutant.

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (3).

Mutational events:

ert-g.24 (NGB 112625, GSHO 479), *-g.80* (NGB 112679), *-g.84* (NGB 112683), *-g.90* (NGB 112689) in Bonus (3); *ert-g.78* (GSHO 480, NGB 112677), *-g.92* (NGB 112691) in Bonus (4); *ert-g.303* (NGB 112820), *-g.349* (NGB 112865), *-g.359* (NGB 112875), *-g.393* (NGB 112910) in Foma (CIho 11333) (7).

Mutant used for description and seed stocks:

ert-g.24 in Bonus (GSHO 479, NGB 112625); *ert-g.24* via Wolfe's Recessive Marker Stock 7.1 in Bowman (PI 483237)*8 (GSHO 2106, BW309, NGB 22105).

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:278.

Revised:

J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:133-134.

BGS 332, Erectoides-r, *Ert-r*

Stock number: BGS 332
Locus name: Erectoides-r
Locus symbol: *Ert-r*

Revised locus symbol:

The *Ert-r.52* is likely an allele at the *Zeo1* (Zeocriton 1) locus based on phenotypic expression and retained SNP markers in 2HL of the Bowman backcross-derived line BW 332 with *Ert-r.52*, the BW937 line with *Zeo1.a*, and the BW938 line with *Zeo1.b* (1). Since the zeocriton phenotype was first described by Hayes and Harlan (4), the recommended locus symbol is *Zeo1*. See BGS 082 for more information the alleles at the *Zeo1* locus.

Previous nomenclature and gene symbolization:

Erectoides-52 = *ert-52* (2).

Inheritance:

Monofactorial incomplete dominant (3).

Located in chromosome 2HL (1), associated with SNP markers 2_0715 to 1_0551 (positions 213.08 to 221.70 cM) in 2HL of the Bowman backcross-derived line BW322, in 2H bin 13 (1).

Description:

Spikes are compact in heterozygotes and very compact in homozygotes, with rachis internode length values from 1.4 to 1.8 mm. Homozygotes are about 2/3 normal height with excellent vigor. The glumes associated with lateral spikelets are 3 to 4 times larger than normal. Lodicule size is reduced (6). Heterozygotes are intermediate in plant height, have slightly more lax spikes, and have normal glumes in lateral spikelets (6). GA₃ treatment of plants as the flag leaf emerges decreases spike density (7).

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763) (2).

Mutational events:

Ert-r.52 (NGB 112651, GSHO 492), *-r.67* (NGB 112666) in Bonus, *-r.329* (NGB 112844) in Foma (CIho 11333) (6); *Ert-r.453* (NGB 112968) in Foma (5).

Mutant used for description and seed stocks:

Ert-r.52 in Bonus (GSHO 492, NGB 112651); *Ert-r.52* in Bowman (PI 483237)*8 (GSHO 2123, BW322, NGB 22117).

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barley. Hereditas 58:359-384.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:280.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:135-136.

BGS 337, Broad leaf 2, *blf2*

Stock number: BGS 337
Locus name: Broad leaf 2
Locus symbol: *blf2*

Previous nomenclature and gene symbolization:

Narrow leaf = *nlh* (4).
Broad leaf 2 = *bb2* (6).
Narrow leaf-k = *nl.k* (2).

Inheritance:

Monofactorial recessive (4).
Located in chromosome 5HL (2); based on linkage drag with the *raw1* (smooth awn 1) locus (2); *blf2.b* is associated with SNP markers 2_0298 to 1_1490 (positions 203.85 to 235.18 cM) 5H bins 11 to 12 of the Bowman backcrossed-derived line BW059 (1).

Description:

Leaf blade width of mutant plants is narrower (about 2/3 of normal) than those of Hannchen (5, 6). Leaf blades of plants of the Bowman backcross-derived line BW059 are 2/3 to 3/4 as wide as those of Bowman. BW059 plants are slightly shorter, have 2 to 3 fewer kernels per spike, and have slightly shorter and lighter kernels. Grain yields of BW059 were similar to those of Bowman (3).

Origin of mutant:

A neutron induced mutant in Hannchen (Clho 531) (5).

Mutational events:

blf2.b in Hannchen (GSHO 1667) (4, 5, 6).

Mutant used for description and seed stocks:

blf2.b in Hannchen (GSHO 1667); *blf2.b* in Bowman (PI 483237)*6 (GSHO 2136), in Bowman*7 (BW059, NGB 20467).

References:

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Prepared:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:285.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:137.

BGS 339, High lysine 3, *lys3*

Stock number: BGS 339
Locus name: High lysine 3
Locus symbol: *lys3*

Previous nomenclature and gene symbolization:

Shrunken endosperm xenia 3 = *sex3* (18, 19).

Inheritance:

Monofactorial recessive (3, 5, 18).

Located in 5HL (9, 13, 20); near the *msg19* (male sterile genetic 19) locus (18); about 14.5 cM proximal from the *fst1* (fragile stem 1) locus; about 20.7 cM proximal from the *ddt1* (reaction to DDT 1) locus (9, 11); likely in the cluster of hordein genes in 1H bin 02. A second variant isolated from Risø 1508 is associated with SNP markers 2_0479 to 3_0918 (positions 0.54 to 17.27 cM) in 1H bins 01 to 02 of the Bowman backcross-derived line BW496 (6).

Description:

After the hard dough stage, kernels develop a depression in the dorsal side or lemma which becomes progressively more distinct with maturity. The 1000-kernel weight of the mutant is about 75% of normal. The mutant expresses xenia permitting classification of kernels from heterozygous plants as normal or shrunken with an expected 3:1 ratio (3). Field establishment and growth of mutant plants is normal (3, 5). Mutant kernels have a higher lysine content than normal kernels (3) and the association with shrunken endosperm is pleiotropic (13, 19). The endosperm is nearly devoid of B- and C-hordeins (8, 14, 16). The B-hordein genes in developing barley endosperm were highly methylated in the *lys3.a* mutant compared to wild-type endosperm (17). A deficiency of kernels with shrunken endosperm occurs in some crosses (1, 2, 5, 18) and was caused likely highly distorted male gamete transmission (4). The gamete lethal factor in Risø 1508 was named *Gam3* (gametophyte factor 3) and was position on 5HL about 6.5 cM from the *lys3* locus (21). Based on SNP mapping information (6), the Bowman backcross-derived line from Risø 1508, BW496, may also contain a shrunken endosperm mutant is near the *Hor2* locus in the 1HS cluster of hordein genes (15), which is not the *lys3.a* mutant. The Bowman backcross-derived line BW496 is apparently more sensitive to environmental stress than Bowman. Heading of BW496 is delayed by 6 to 10 days, plants are 2/3 to almost normal in height, and peduncles are 1/2 to normal in length. Kernel weights for BW496 were 30% lower than those for Bowman. Grain yields of BW496 were about half of normal (7).

Origin of mutant:

An induced mutant in Bomi (PI 43371) (3).

Mutational events:

lys3.a in Bomi (Risø 1508, GSHO 1785) (3, 9); *lys3.b* (Risø 18), *lys3.c* (Risø 19) in Bomi (9, 12).

Mutant used for description and seed stocks:

lys3.a in Bomi (GSHO 1785); a second mutant from Risø 1508 in Bowman (PI 483237)*6 (BW496, NGB 20724).

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Prepared:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:287-288.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:138-139.

BGS 343, Leafy bract 1, *Lfb1*

Stock number: BGS 343
Locus name: Leafy bract 1
Locus symbol: *Lfb1*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial dominant (3) with variable expressivity.
Located in chromosome 5HL (4); about 7.5 cM from the *srh1* (short rachilla hair 1) locus (4); *Lfb1.a* is associated with SNP markers 2_0645 to 2_0850 (positions 134.85 to 157.13 cM) in 5H bins 08 to 09 of the Bowman backcross-derived line BW478 (1).

Description:
A leaf-like bract forms at the collar below the spike. The size of the leaf-like bract may vary from vestigial to 5 cm or longer (3, 4). Tiller to tiller variation in bract size occurs and the bract is often larger in cultivars having six-rowed spikes (2). The agronomic and morphological traits of Bowman backcross-derived line for the *Lfb1.a* mutant, BW478, were similar to those of Bowman (2).

Origin of mutant:
An induced mutant in Montcalm (Clho 7149) (3).

Mutational events:
Lfb1.a (GSHO 1577) in Montcalm (3).

Mutant used for description and seed stocks:
Lfb1.a in Montcalm (GSHO 1577); *Lfb1.a* in Bowman*7 (GSHO 2152, BW478, NGB 20706).

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Prepared:
J.D. Franckowiak. 1998. *Barley Genet. Newsl.* 28:30.

Revised:
J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:140.

BGS 352, Glossy sheath 2, *gsh2*

Stock number: BGS 352
Locus name: Glossy sheath 2
Locus symbol: *gsh2*

Previous nomenclature and gene symbolization:

Glossy sheath 2 = *gs2* (18, 20).

Eceriferum-b = *cer-b* (8, 20).

Inheritance:

Monofactorial recessive (8, 17).

Located in chromosome 3HL (2, 4, 19); about 5.1 cM proximal from the *als1* (absent lower laterals 1) locus (5, 6); over 32.5 cM distal from the *uzu1* (*uzu* 1) locus (2, 5, 6); *gsh2.f* is associated with SNP markers 2_1161 to 1_0584 (positions 169.94 to 178.12 cM) in 3H bin 11 of the Bowman backcross-derived line BW405; *cer-b.2* is associated with SNP markers 22_1513 to 1_1172 (positions 190.97 cM) in 3H bins 11 and 12 of the Bowman backcross-derived line BW107 (1), in 3H bin 11.

Description:

Surface wax coating appears absent on the spike, leaf sheath, and stem (wax code - - ++) (8, 17). The Bowman backcross-derived lines for the *gsh2* mutants, BW107 with *cer-b.2* and BW405 with *gsh2.f*, had agronomic traits similar to those of Bowman, but grain yields were slightly lower (3).

Origin of mutant:

Spontaneous occurrence in Vantage (Clho 7324) (16); an X-ray induced mutant in Maja (PI 184884) (8).

Mutational events:

gsh2.d in Vantage, *gsh2.e* in Ymer (Clho 7275), *gsh2.f*, *gsh2.g* (GSHO 736) in Atlas (Clho 4118), *gsh2.h* in Klargrin (16); *cer-b.2* (NGB 110886, GSHO 434; GSHO 1081) in Maja (7, 8, 9, 20); *cer-b.4* (NGB 110888), *-b.64* (NGB 110948), *-b.66* (NGB 110950), *-b.109* (NGB 110994 in Bonus (PI 189763) (8, 9); *cer-b.79* (NGB 110963), *-b.94* (NGB 110978), *-b.96* (NGB 110980) in Bonus, *-b.209* (NGB 111096), *-b.222* (NGB 111109), *-b.319* (NGB 111206), *-b.336* (NGB 111223), *-b.337* (NGB 111224), *-b.377* (NGB 111264), *-b.418* (NGB 111306), *-b.424* (NGB 111312), *-b.427* (NGB 111315) in Foma (Clho 11333) (9, 15); *cer-b.169* (NGB 111055), *-b.193* (NGB 111079) in Bonus, *-b.412* (NGB 111300), *-b.531* (NGB 111419), *-b.549* (NGB 111437) in Foma, *-b.1037* (NGB 111925), *-b.1059* (NGB 111947) in Carlsberg II (Clho 10114) (9); *cer-b.751* (NGB 111639), *-b.769* (NGB 111657), *-b.791* (NGB 111679), *-b.799* (NGB 111687), *-b.800* (NGB 111688) in Bonus, *-b.1129* (NGB 112017) in Kristina (NGB 1500) (10); *cer-b.910* (NGB 111798) in Bonus (11); *cer-b.932* (NGB 111820) in Bonus (12); *cer-b.147* (NGB 111033), *-b.182* (NGB 111068), *-b.623* (NGB 111511) in Bonus, *-b.1099* (NGB 111987), *-b.1267* (NGB 112155), *-b.1269* (NGB 112157) in Kristina (13); *cer-b.1699* (NGB 117326) in Bonus (14); *gsh2.ab* (OUM019), *gsh2.ah* (OUM025) in Akashinriki (OUJ659, PI 467400) (4, 6); *gsh2.bb* in the cross NDB112/Fr926-77 (3).

Mutant used for description and seed stocks:

gsh2.f in Atlas (GSHO 736); *cer-b.2* in Maja (NGB 110886, GSHO 434; GSHO 1081); *gsh2.f* in Bowman (PI 483237)*7 (GSHO 1988), in Bowman*8 (BW405, NGB 20638); *cer-b.2* in Bowman*6 (GSHO 1989), in Bowman*7 (BW107, NGB 20513).

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Prepared:

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Revised:

- U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:294-295.
 U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:141-142.

BGS 353, Glossy sheath 3, *gsh3*

Stock number: BGS 353
Locus name: Glossy sheath 3
Locus symbol: *gsh3*

Previous nomenclature and gene symbolization:

Glossy sheath 3 = *gs3* (22).
Eceriferum-a = *cer-a* (6, 19).

Inheritance:

Monofactorial recessive (6, 16).
Located in chromosome 7HS (3, 16, 21, 22); about 2.1 cM proximal from the *fch12* (chlorina seedling 12) locus (18); and 6.5 to 12.9 cM proximal from the *brh1* (brachytic 1) locus (17, 18, 20); *gsh3.i* is associated with SNP markers 1_0498 to 2_1144 (positions 81.43 to 113.28 cM) in 7H bin 02 of the Bowman backcross-derived line BW406 (1), in 7H bin 02.

Description:

Surface wax coating appears absent on the spike, leaf sheath, and stem (wax code - - ++) (6, 16, 22). Based on the chemical epicuticular wax composition, only traces of the β -Bonus (23, 24). A reduction in the long-chain n-alkanes occurs in the *cer-a.6* mutant without affecting the chain-length distributions of the minor hydrocarbons (25). Compared to Bowman, the Bowman backcross-derived line with *gsh3.i*, BW406, had slightly small kernels that weighed 10 to 20% less. The grain yields of BW406 were 1/2 to 2/3 those of Bowman (4). diketone wax classes and alkan-2-ol containing esters occur in the *cer-a.6* mutant of

Origin of mutant:

A radiation induced mutant in Mars (CIho 7015) (16, 21, 22); an X-ray induced mutant in Maja (PI 184884) (6).

Mutational events:

gsh3.i (GSHO 737) in Mars (15, 16); *gsh3.j* in Chevron (CIho 1111), *gsh3.k* in a hybrid between Atlas and Algerian (15); *cer-a.1* (NGB 110885, GSHO 422) in Maja (2, 6, 7); *cer-a.6* (NGB 110890), -a.12 (trans) (NGB 110896), -a.33 (NGB 110917) in Bonus (PI 189763) (6, 7); *cer-a.98* (trans) (NGB 110982), -a.121 in Bonus (NGB 111006), -a.207 (NGB 111094), -a.215 (NGB 111102), -a.224 (NGB 111111), -a.225 (NGB 111112), -a.235 (NGB 111122), -a.242 (NGB 111129), -a.276 (NGB 111163), -a.302 (NGB 111189), -a.329 (NGB 111216), -a.503 (NGB 111391) in Foma (CIho 11333) (7, 14); *cer-a.134* (NGB 111019), -a.190 (NGB 111076), -a.191 (NGB 111077), -a.192 (NGB 111078), -a.682 (NGB 111570) in Bonus, -a.224 (NGB 111111), -a.534 (NGB 111422), -a.539 (NGB 111427) in Foma, -a.1007 (NGB 111895), -a.1013 (NGB 111901), -a.1021 (NGB 111909), -a.1028 (NGB 111916), -a.1050 (NGB 111938), -a.1051 (NGB 111939) in Carlsberg II (CIho 10114) (7); *cer-a.154* (NGB 111040), -a.160 (NGB 111046), -a.750 (NGB 111638), -a.857 (NGB 111745), -a.862 (NGB 111750), -a.863 (NGB 111751) in Bonus (8); *cer-a.836* (NGB 111724), -a.873 (NGB 111761), -a.896 (NGB 111784), -a.916 (NGB 111804) in Bonus, -a.1194 (NGB 112082) in Kristina (NGB 1500) (9); *cer-a.1197* (NGB 112085), -a.1249 (NGB 112137), -a.1250 (NGB 112138) in Kristina (10); *cer-a.1199* (NGB 112087), -a.1308 (NGB 112196), -a.1336 (NGB 112224), -a.1347 (NGB 112235) in Kristina (11); *cer-a.913* (NGB 111801), -a.1394 (NGB 112282), -a.1461 (NGB 112349), -a.1463 (NGB 112351) in Bonus, -a.1509 (NGB 112397), -a.1513 (NGB 112401) in Nordal (12); *cer-a.1524* (NGB 112412), -a.1530 (NGB 112418), -a.1531 (NGB 112419), -a.1554 (NGB 112442), -a.1557 (NGB 112445) in Nordal, -a.1704 (NGB 112517), -a.1750 (NGB 112564), -a.1774 (NGB 112589), -a.1788 (NGB

117334) in Bonus (13); *gsh3.af* (OUM023), *gsh3.aj* (OUM027) in Akashinriki (PI 467400, OUJ659) (5).

Mutant used for description and seed stocks:

gsh3.i in Mars (GSHO 737); *cer-a.1* in Maja (GSHO 422, NGB 110885); *gsh3.i* via R.I. Wolfe's Multiple Marker Stock for Chromosome 1 in Bowman (PI 483237)*8 (GSHO 1825, BW406, NGB 20639; *cer-a.1* (NGB 110885) in Maja was used for allelism tests; *cer-a.6* (NGB 110890) in Bonus was used for wax chemistry and wax structure studies (23, 24).

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Prepared:

W.L. McProud and R.F. Eslick. 1971. *Barley Genet. Newsl.* 1:169-170.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:296-297.

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:143-145.

BGS 354, Glossy sheath 4, *gsh4*

Stock number: BGS 354
Locus name: Glossy sheath 4
Locus symbol: *gsh4*

Previous nomenclature and gene symbolization:

Glossy sheath 4 = *gs4* (19).

Eceriferum-x = *cer-x* (7).

Inheritance:

Monofactorial recessive (7, 19).

Located in chromosome 6HL (17, 18, 19), near the centromere and less than 3.0 cM distal from the *rob1* (orange lemma 1) locus (2, 3, 5); *gsh4.l* and *rob1.a* is associated with SNP markers 1_0355 to 2_0118 (positions 73.90 to 156.09 cM) of 6H bins 06 to 09 in Bowman backcross-derived line BW407; *cer-x.60* is associated with SNP markers 2_0675 to 2_0118 (positions 82.43 to 156.09 cM) of 6H bins 06 to 09 in Bowman backcross-derived line BW126 (1), likely in 6H bin 06 proximal from the *rob1* locus.

Description:

Surface wax coating appears absent on the spike, leaf sheath, and stem (wax code - - ++) (7, 17). Only traces of the β -diketone wax classes and alkan-2-ol containing esters occurred in the *cer-x.60* mutant based on evaluation of the chemical epicuticular wax composition (20, 21). A reduction in the long-chain n-alkanes occurs in the *cer-x.60* mutant without affecting the chain-length distributions of the minor hydrocarbons (22). Kernel weights for the Bowman backcross-derived lines, BW126 with *cer-x.60* and BW407 with *gsh4.l*, were often about 10% less than those for Bowman. Grain yields averaged about 3/4 those of Bowman (4).

Origin of mutant:

A radiation induced mutant in Gateway (Clho 10072) (16, 17); an ethylene imine induced mutant in Bonus (PI 189763) (7).

Mutational events:

gsh4.l (GSHO 738) in Gateway (16, 17); *cer-x.60* (NGB 110944, GSHO 1520) in Bonus (6, 7, 8, 16); *cer-x.102* (NGB 110987), *-x.114* (NGB 110999) in Bonus, *-x.228* (GSHO 445, NGB 111118), *-x.309* (NGB 111196), *-x.350* (NGB 111237), *-x.417* (NGB 111305), *-x.449* (NGB 111337), *-x.450* (NGB 111338), *-x.507* (NGB 111395) in Foma (Clho 11333) (8, 15); *cer-x.164* (NGB 110015), *-x.658* (NGB 111546) in Bonus, *-x.561* (NGB 111449) in Foma, *-x.1049* (NGB 111933), *-x.1055* (NGB 111943), *-x.1066* (NGB 111954) in Carlsberg II (Clho 10114) (8); *cer-x.788* (NGB 111676) in Bonus, *-x.1095* (NGB 111983) in Kristina (NGB 1500) (9); *cer-x.1180* (NGB 112068) in Kristina (10); *cer-x.1236* (NGB 112124) in Kristina (11); *cer-x.886* (NGB 111774) in Bonus (12); *cer-x.1398* (NGB 112286), *-x.1435* (NGB 112323) in Bonus, *-x.1508* (NGB 112396) in Nordal (13); *cer-x.1000* (NGB 111888), *-x.1498* (NGB 112386) in Bonus, *-x.1518* (NGB 112406), *-x.1523* (NGB 112411), *-x.1529* (NGB 112417), *-x.1536* (NGB 112424), *-x.1547* (NGB 112435), *-x.1552* (NGB 112440) in Nordal, *-x.1732* (NGB 112545), *-x.1756* (NGB 112571) in Bonus (14).

Mutant used for description and seed stocks:

gsh4.l in Gateway (GSHO 738); *cer-x.60* in Bonus (GSHO 1520, NGB 110944); *gsh4.l* via R.I. Wolfe's Multiple Maker Stock for Chromosome 6H in Bowman (PI 483237)*7 (GSHO 2072, BW407, NGB 20640); *cer-x.60* in Bowman*7 (GSHO 2073, BW126, NGB 20532).

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Prepared:

W.L. McProud and R.F. Eslick. 1971. *Barley Genet. Newsl.* 1:170-171.

U. Lundqvist. 1975. *Barley Genet. Newsl.* 5:134 as BGS 416, *Eceriferum*-x, *cer*-x.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:298-299.
U. Lundqvist and J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:146-148.

BGS 355, Glossy sheath 5, *gsh5*

Stock number: BGS 355
Locus name: Glossy sheath 5
Locus symbol: *gsh5*

Previous nomenclature and gene symbolization:

Glossy sheath 5 = *gs5* (14).
Eceriferum-s = *cer-s* (4, 12).
Glossy sheath 8 = *gs8* (16).

Inheritance:

Monofactorial recessive (4).
Located in chromosome 2HL (14, 15, 16, 18); in the centromeric region about 2.5 cM proximal from the *eog1* (elongated outer glume 1) locus (14, 16); about 32.0 cM proximal from the *vsr1* (six-rowed spike 1) locus (14, 16); *gsh5.m* is associated with SNP markers 1_0851 to 2_1437 (positions 81.43 to 113.28 cM) in 2H bins 06 to 08 of the Bowman backcross-derived line BW408 (1); *cer-s.31* is associated with SNP markers 1_0796 to 2_0528 (positions 95.53 to 118.78 cM) in 2H bins 07 to 08 of the Bowman backcross-derived line BW122 (1), in 2H bin 07.

Description:

Mutants have a reduced surface wax covering on the spikes and stems, and a bright glossy green color on all leaf sheaths (14) (wax code + - ++ (4). The nodes appear to have an excessive wax covering (3). The Bowman backcross-derived line with the *cer-s.31* allele, BW122, headed 2 to 4 days later than BW408 with the *gsh5.m* allele and Bowman (3). BW122 also had 3 to 6 more kernels per spike. Kernels of BW122 and BW408 were about 10% lighter than those of Bowman. The grain yields of BW408 were often slightly lower than those of Bowman or BW408 (3). The differences in maturity and number of kernels per spike between BW122 and BW408 were attributed to close linkage between alleles at the *gsh5* locus and those at the *Eam6* (early maturity 6 or earliness per se QTL 2S = *eps2S*) locus (3).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (4); a radiation induced mutant in Jotun (PI 467357) (14); a spontaneous mutant in Okaiku 3 (OUL011) (17).

Mutational events:

cer-s.24 (NGB 110908) in Bonus (4); *cer-s.31* (NGB 110915, GSHO 440) in Bonus (2, 4); *cer-s.41* (NGB 110925) in Bonus (4); *cer-s.287* (NGB 111174), *-s.303* (NGB 111190), *-s.372* (NGB 111259), *-s.444* (NGB 111332) in Foma (Clho 11333) (12); *cer-s.1047* (NGB 111935) in Carlsberg II (Clho 10114) (5); *cer-s.137* (NGB 111022) in Bonus, *-s.591* (NGB 111479) in Foma, *-s.803* (NGB 111691) in Bonus, *-s.1132* (NGB 112020) in Kristina (NGB 1500) (6); *cer-s.914* (NGB 111802) in Bonus (7); *cer-s.622* (NGB 111510) in Bonus, *-s.1054* (NGB 111942) in Carlsberg II, *-s.1153* (NGB 117264) in Kristina (8); *cer-s.1323* (NGB 112211) in Bonus (9); *cer-s.1134* (NGB 112022) in Kristina (10); *cer-s.1754* (NGB 112554) in Bonus (11); *gsh5.m* (GSHO 739) in Jotun (14); *gsh5.n* in Okaiku 3 (GSHO 832) (13, 17).

Mutant used for description and seed stocks:

gsh5.m in Jotun (GSHO 739); *cer-s.31* in Bonus (GSHO 440, NGB110915); *cer-s.31* in Bowman (PI 483237)*5 (GSHO 1888), in Bowman*8 (BW122, NGB 20528); *gsh5.m* in Bowman*8 (GSHO 1889, BW408, NGB 20641).

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Revised:

J.D. Franckowiak and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:300-301.

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:149-150.

BGS 387, Desynapsis 8, *des8*

Stock number: BGS 387
Locus name: Desynapsis 8
Locus symbol: *des8*

Previous nomenclature and gene symbolization:
None.

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 3H (3); *des8.l* is associated with SNP markers 1_0281 to 2_0168 (positions 98.41 to 173.82 cM) in 3H bins 06 to 11 of the Bowman backcross-derived line BW248 (1); *des8.k* is associated with SNP markers 1_1401 to 2_1493 (positions 89.73 to 161.43 cM) in 3H bins 06 to 11 of the Bowman backcross-derived line BW247 (1). Both BW247 and BW248 also retained several SNP marker heterogeneities around SNP marker 2_0247 (position 159.73 cM) in 7H bin 11 (1).

Description:

The chromosomes are paired during pachytene and undergo desynapsis during diplotene. The degree of desynapsis was 7.9 ± 2.3 , ranging from 7 ring bivalents ($d = 0$) to 14 univalents ($d = 14$). Many univalents split longitudinally during anaphase I. Lagging chromosomes and micronuclei were frequently observed at telophase I. Microspore quartets contained an average of 1.2 micronuclei per quartet with a range of 0 to 10. Ovule fertility was about 43% in the *des8.k* stock, but only about 1% in the *des8.l* stock (3). Plants of the Bowman backcross-derived line for *des8.l*, BW248, produced very little seed in most trials, but in one experiment grain yields were 3/4 those of Bowman. Kernels of BW248 were slightly longer than those of Bowman, but weighed about 10% less (2).

Origin of mutant:

A spontaneous mutant in Betzes (PI 129430) (4, 5).

Mutational events:

des8.k (GSHO 599), *des8.l* in Betzes (4, 5).

Mutant used for description and seed stocks:

des8.k in Betzes (GSHO 599); *des8.k* in Bowman*3 (BW247, NGB 22073); *des8.l* in Bowman*5 (BW248, NGB 22471).

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Prepared:

J.M. Hernandez-Soriano, R.T. Ramage, and R.F. Eslick. 1973. *Barley Genet. Newsl.* 3:131.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:335.
J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:151.

BGS 389, Desynapsis 10, *dsp10*

Stock number: BGS 389
Locus name: Desynapsis 10
Locus symbol: *des10*

Previous nomenclature and gene symbolization:

Desynapsis p = *des*,,p (3, 5).

Inheritance:

Monofactorial recessive (3, 5).

Located in chromosome 5HL (1); *des10.p* is associated with SNP markers 2_0127 to 12_0259 (positions 189.08 to 203.85 cM) in 5H bins 10 to 11 of the Bowman backcross-derived line BW230 (1).

Description:

The chromosomes are paired during pachytene and undergo desynapsis during diplotene and diakinesis. The average degree of desynapsis was 2.0, ranging from 7 ring bivalents ($d = 0$) to 3 ring bivalents plus 2 rod bivalents plus 4 univalents ($d = 6$). Ovule fertility was 60 to 80% (4). Plants of the Bowman backcross-derived line for *des10.p*, BW230, were similar to Bowman except that reduced seed set decreased grain yields to about half those for Bowman (2).

Origin of mutant:

A spontaneous mutant in Betzes (PI 129430) (5).

Mutational events:

des10.p (GSHO 601) in Betzes (3, 5).

Mutant used for description and seed stocks:

des10.p in Betzes (GSHO 601); *des10.p* in Bowman*6 (BW230, NGB 22057).

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Prepared:

J.M. Hernandez-Soriano and R.T. Ramage. 1974. *Barley Genet. Newsl.* 4:138.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:337.

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 41:152.

BGS 399, Eceriferum-d, *cer-d*

Stock number: BGS 399
Locus name: Eceriferum-d
Locus symbol: *cer-d*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (3).
Location in 5HL (1); *cer-d.5* is associated with SNP markers 1_0104 to 2_1452 (positions 223.57 to 244.39 cM) in 5H bins 11 to 12 of the Bowman backcross-derived line BW108 (1), likely in 5H bin 12.

Description:
Surface wax coating on the spike is reduced (wax code + ++ ++) (3). A translocation is present in the mutant stock *cer-d.5*, but it is not linked to the *cer-d* locus. The original stock has a lax spike and heads early (3, 9). Plants of the Bowman backcross-derived line for *cer-d.5*, BW108, showed shorter, narrower leaf blades and reduced plant vigor, but they headed two days earlier than Bowman. Compared to Bowman, BW108 plants and their awns were slightly shorter, rachis internodes were slightly longer, kernels were slightly longer and narrower, and they weighted 10 to 20% less. The BW108 lodged easily and grain yield were about 10% lower than those of Bowman (2).

Origin of mutant:
An X-ray induced mutant in Bonus (PI 189763) (3).

Mutational events:
cer-d.5 (trans) (NGB 110889, GSHO 425), *-d.40* (NGB 110924), *-d.104* (NGB 110989) in Bonus (3, 4); *cer-d.111* (NGB 110996), *-d.149* (NGB 111035) in Bonus (4, 9); *cer-d.713* (NGB 111601) in Bonus (4); *cer-d.809* (NGB 111697), *-d.826* (NGB 111714) in Bonus (5); *cer-d.965* (NGB 111873) in Bonus (6); *cer-d.712* (NGB 111600), *-d.1326* (NGB 112214) in Bonus (7); *cer-d.1818* (NGB 117316), *-d.1819* (NGB 117367), *-d.1820* (NGB 117368) in Bonus (8).

Mutant used for description and seed stocks:
cer-d.5 in Bonus (GSHO 425, NGB 110889); *cer-d.5* in Bowman (PI 483237)*5 (GSHO 2189), in Bowman *6 (BW108, NGB 20514).

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Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:346.

U. Lundqvist and J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:153-154.

BGS 402, Eceriferum-g, *cer-g*

Stock number: BGS 402
Locus name: Eceriferum-g
Locus symbol: *cer-g*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (4).
Located in chromosome 2HL (2, 14); about 15.9 cM distal from the *vrs1* (six-rowed spike 1) locus (14, 15); *cer-g.10* is associated with SNP markers 1_0317 to 2_0374 (positions 98.35 to 104.81 cM) in 2H bin 08 and SNP markers 1_0619 to 1_0533 (positions 133.59 to 141.56 cM) in 2H bin 09 of the Bowman backcross-derived line BW111 (1), in 2H bin 08.

Description:
Mutants have reduced surface wax coating on spike, leaf sheath, and stem (wax code + + ++) with the wax coating of the leaf sheath and stem wax present in broad horizontal bands (4). Double and triple stomatal complexes are produced during stomatal development (4, 16). All *cer-g* mutants have globe-shaped or globosum kernels (4). Plants of the Bowman backcross-derived line for *cer-g.10*, BW111, headed 1 to 2 days later than Bowman and about 10% shorter. Kernels of BW111 were shorter (8.2 vs. 9.5 mm), narrower (3.5 vs. 3.8 mm) and weighed 15 to 20% less. Grain yields of BW111 were 2/3 to 3/4 those of Bowman (3).

Origin of mutant:
An X-ray induced mutant in Bonus (PI 189763) (4).

Mutational events:
cer-g.10 (NGB 110894, GSHO 428), *-g.11* (NGB 110895), *-g.23* (NGB 110907), *-g.47* (NGB 110931), *-g.55* (NGB 110939) in Bonus (4); *cer-g.106* (NGB 110991) in Bonus, *-g.202* (NGB 111089), *-g.208* (NGB 111095), *-g.210* (NGB 111097), *-g.494* (NGB 111382) in Foma (Clho 11333) (13); *cer-g.166* (NGB 111052) in Bonus, *-g.553* (NGB 111441), *-g.568* (NGB 111456), *-g.700* (NGB 111588), *-g.709* (NGB 111546), *-g.710* (NGB 111597) in Foma, *-g.1026* (NGB 111914) in Carlsberg II (Clho 10114) (5); *cer-g.746* (NGB 111634), *-g.818* (NGB 111706), *-g.875* (NGB 111763) in Bonus, *-g.1033* (NGB 111921), *-g.1071* (NGB 111959) in Carlsberg II, *-g.1097* (NGB 111985), *-g.1116* (NGB 112004) in Kristina (NGB 1500) (6); *cer-g.893* (NGB 111781), *-g.976* (NGB 111864) in Bonus, *-g.1172* (NGB 112060) in Kristina (7); *cer-g.1161* (NGB 117268), *-g.1169* (NGB 112057) in Kristina (8); *cer-g.1038* (NGB 111926) in Carlsberg II, *-g.1289* (NGB 111177) in Kristina, *-g.1332* (NGB 112220) in Bonus (9); *cer-g.1410* (NGB 112298), *-g.1451* (NGB 112339), *-g.1454* (NGB 112342) in Bonus (10); *cer-g.1495* (NGB 112383) in Bonus, *-g.1510* (NGB 112398) in Nordal, *-g.1736* (NGB 112549, 117328), *-g.1740* (NGB 112553), *-g.1741* (NGB 112554) in Bonus (11); *cer-g.1573* (NGB 112461) in Nordal (12).

Mutant used for description and seed stocks:
cer-g.10 in Bonus (GSHO 428, NGB 110894); *cer-g.10* in Bowman (PI 483237)*6 (GSHO 1906), in Bowman*7 (BW111, NGB 20517).

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BGS 403, Eceriferum-h, *cer-h*

Stock number: BGS 403
Locus name: Eceriferum-h
Locus symbol: *cer-h*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (3).
Located in chromosome 4HS (1); *cer-h.13* is associated with SNP markers 2_1056 to 2_0210 (positions 5.24 to 38.41 cM) in 4H bins 01 to 04 of the Bowman backcross-derived line BW112 (1).

Description:
Surface wax coating on the spike appears absent (wax code - ++ ++) (3). The original stock has wide leaves, pointed lateral spikelets, and a high level of sterility (10 to 25% seed set). In the Bowman backcross-derived line, BW112, plants are semidwarf (about 80% of normal height) and have short, slightly lax spikes with reduced seed set. The original *cer-h.13* stock may have a translocation (2), but sterility in the Bowman stock is not associated with a translocation. The kernels of BW112 plants were 20 to 30% lighter than those of Bowman; and seed yields were very low (2).

Origin of mutant:
An X-ray induced mutant in Bonus (PI 189763) (3).

Mutational events:
cer-h.13 (trans) (NGB 110897, GSHO 429) in Bonus (3, 4); *cer-h.125* (NGB 111010), in Bonus (4); *cer-h.233* (NGB 111120), *-h.355* (NGB 111242) in Foma (Clho 11333) (4, 7); *cer-h.721* (NGB 117259) in Bonus (5); *cer-h.1698* (NGB 112557) in Bonus (6).

Mutant used for description and seed stocks:
cer-h.13 in Bonus (GSHO 429, NGB 110897); *cer-h.13* in Bowman (PI 483237)*5 (GSHO 2190), in Bowman*7 (BW112, NGB 20518).

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Prepared:
U. Lundqvist. 1975. *Barley Genet. Newsl.* 5:121.

Revised:
U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:351.
U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:157.

BGS 404, Eceriferum-i, *cer-i*

Stock number: BGS 404
Locus name: Eceriferum-i
Locus symbol: *cer-i*

Previous nomenclature and gene symbolization:
None.

Inheritance:

Monofactorial recessive (2).

Located in chromosome 5HL (2, 12); about 5.6 cM distal from the *ari-e* (breviaristatum-e) locus (2, 13, 14); *cer-i.16* is associated with SNP markers 2_0206 to 2_0449 (positions 9.61 to 154.37 cM) in 5H bins 01 to 09 of the Bowman backcross-derived line BW113 (1), likely in 5H bins 08 or 09.

Description:

Surface wax coating on the spike appears absent (wax code - ++ ++) (4). A translocation is present in the *cer-i.25* stock, with one of the breakpoints being close to the *cer-i* locus (4). Concerning epicuticular wax composition, the wax tubes are much shorter in the mutant, and the amount of two types of diketones (β -diketone and hydroxy- β -diketone) is proportionally reduced (15, 16, 17). Plants of the Bowman backcross-derived line for *cer-i.16*, BW113, were similar to Bowman in agronomic traits (3).

Origin of mutant:

An alpha-ray induced mutant in Bonus (PI 189763) (4).

Mutational events:

cer-i.16 (NGB 110900, GSHO 430), *-i.25* (trans) (NGB 110909), *-i.27* (NGB 110911), *-i.30* (NGB 110914), *-i.32* (NGB 110916), *-i.45* (NGB 110929), *-i.51* (NGB 110935), *-i.112h* (NGB 110997), *-i.112l* (NGB 111087) in Bonus (4, 5); *cer-i.92* (NGB 110976), *-i.110* (NGB 110995) in Bonus (5, 11); *cer-i.156* (NGB 111042), *-i.168* (NGB 111054), *-i.195* (NGB 111081) in Bonus (3); *cer-i.205* (NGB 111092), *-i.212* (NGB 111099), *-i.255* (NGB 111142), *-i.256* (NGB 111143), *i.257* (NGB 111144), *-i.263* (NGB 111150), *-i.415* (NGB 111303), *-i.419* (NGB 111307), *-i.430* (NGB 111318), *-i.435* (NGB 111323), *-i.477* (NGB 111365), *-i.486* (NGB 111374) in Foma (Clho 11333) (5, 11); *cer-i.426* (NGB 111314), *-i.434* (NGB 111322), *-i.535* (NGB 111423), *-i.554* (NGB 111442) in Foma, *-i.651* (NGB 111539), *-i.653* (NGB 117258), *-i.655* (NGB 111543), *-i.679* (NGB 111567), *-i.702* (NGB 111590), *-i.704* (NGB 111592), *-i.720* (NGB 111608), *-i.722* (NGB 117259), *-i.732* (NGB 111620, 117260), *-i.734* (NGB 111622), *-i.740* (NGB 111628) in Bonus (5); *cer-i.802* (NGB 111690), *-i.805* (NGB 111693), *-i.811* (NGB 111699), *-i.814* (NGB 111702), *-i.867* (NGB 111755), *-i.878* (NGB 111766) in Bonus (6); *cer-i.747* (NGB 111635), *-i.894* (NGB 111802), *-i.921* (NGB 111809), *-i.922* (NGB 111810), *-i.927* (NGB 111815), *-i.928* (NGB 111816), *-i.936* (NGB 11124), *-i.958* (NGB 111846) in Bonus, *-i.1175* (NGB 112063), *-i.1181* (NGB 112069) in Kristina (NGB 1500) (6); *cer-i.891* (NGB 111799), *-i.953* (NGB 111841) in Bonus, *-i.1196* (NGB 112084), *-i.1220* (NGB 112108), *-i.1257* (NGB 112154) in Kristina (7); *cer-i.1354* (NGB 112242) in Bonus (8); *cer-i.1397* (NGB 112285), *-i.1711* (NGB 112524), *-i.1743* (NGB 112556), *-i.1823* (NGB 116832, 117371) in Bonus (9); *cer-i.1764* (NGB 112579) in Bonus (10).

Mutant used for description and seed stocks:

cer-i.16 in Bonus (GSHO 430, NGB 110900); *cer-i.25* in Bonus is used for allelism tests; *cer-i.16* in Bowman (PI 483237)*7 (GSHO 2112, BW113, NGB 20519).

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 7. Lundqvist, U., and D. von Wettstein. 1975. Stock list for the eceriferum mutants III. *Barley Genet. Newsl.* 5:88-91.
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Prepared:

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Revised:

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U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:158-159.

BGS 405, Eceriferum-k, *cer-k*

Stock number: BGS 405
Locus name: Eceriferum-k
Locus symbol: *cer-k*

Previous nomenclature and symbolization:
None.

Inheritance:
Monofactorial recessive (4).
Located in chromosome 4HL (1); *cer-k.39* is associated with SNP markers 1_0387 to 1_1019 (positions 179.78 to 183.54 cM) in 4H bins 12 to 13 of the Bowman backcross-derived line BW115 (1). Previously located in 7HS, based on a linkage drag association with the *ant1* (anthocyanin-less 1) locus (3).

Description:
Surface wax coating on the spike is slightly reduced compared to the parent (wax code + ++ ++) (4). In the Bowman backcross-derived line for *cer-k.39*, BW115, leaf blades and kernels appeared slightly thinner compared to those of Bowman (2). BW115 plants headed 5 to 10 days later than Bowman and were slightly shorter, but they had up to 5 more kernels per spike. Kernel weights of BW115 were 10 to 15% lower and grain yields were about 75% of the Bowman yields (2).

Origin of mutant:
An X-ray induced mutant in Bonus (PI 189763) (4).

Mutational events:
cer-k.39 in Bonus (NGB 110923, GSHO 432) (4, 5).

Mutant used for description and seed stocks:
cer-k.39 in Bonus (GSHO 432, NGB 110923; *cer-k.39* in Bowman (PI 483237)*6 (GSHO 1837), in Bowman*7 (BW115, NGB 20521).

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Prepared:
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Revised:
U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:354.
U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:160.

BGS 407, Eceriferum-m, *cer-m*

Stock number: BGS 407
Locus name: Eceriferum-m
Locus symbol: *cer-m*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Location in chromosomes 1HL or 3HL (1), based on SNP markers retained in the Bowman backcross-derived line BW117 for *cer-m.15*, between 2_0229 to 2_1126 (positions 106.61 to 110.10 cM) in 1H bin 10 and between 1_0918 and 1_1172 (positions 187.28 to 190.87 cM) in 3H bin 12 (1).

Description:

Surface wax coating on the spike appears reduced or normal, and the wax coating on the leaf sheath and stem is reduced (wax code +/++ + ++) (3, 5). The mutant is a semidwarf (3/4 to 5/6 of normal height) and may be semi-sterile (25 to 50% seed set) (3). Rachis internodes of plants in Bowman backcross-derived line BW117 plants were slightly shorter than those of Bowman. The number of kernels per spike for BW117 was 4 or 6 fewer than for Bowman. Kernel weights and test weights were 10 to 20% lower. Seed yields of BW117 were about 1/3 of those of Bowman (2).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (3).

Mutational events:

cer-m.15 (NGB 110899, GSHO 434) in Bonus (3, 4).

Mutant used for description and seed stocks:

cer-m.15 in Bonus (GSHO 434, NGB 110889); *cer-m.15* in Bowman (PI 483237)*6 (GSHO 2192, BW117, NGB 20523).

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5. Lundqvist, U., P. von Wettstein-Knowles, and D. von Wettstein. 1968. Induction of eceriferum mutants in barley by ionizing radiations and chemical mutagens. II. *Hereditas* 59:473-504.

Prepared:

U. Lundqvist. 1975. *Barley Genet. Newsl.* 5:125.

Revised:

- U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:356.
U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:161.

BGS 410, Eceriferum-p, *cer-p*

Stock number: BGS 410
Locus name: Eceriferum-p
Locus symbol: *cer-p*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 7HL (1); *cer-p.43* is associated with SNP markers 11_0174 to 1_0547 (positions 229.66 to 232.00 cM) in 7H bins 13 to 14 of the Bowman backcrossed-derived line BW120 (1).

Description:

Surface wax coating on the leaf blade appears reduced (wax code ++ ++ +) (4). Concerning the chemical epicuticular wax composition, a new form of wax crystals, lobe shaped bodies, were observed in the leaf blade. The amount of wax per unit surface area is reduced, but the wax class distribution is the same as in the wild type (3, 12, 13). The Bowman backcross-derived line containing *cer-p.43*, BW120, was morphological and agronomically similar to Bowman in trials (2).

Origin of mutant:

A gamma-ray induced mutant in Bonus (PI 189763) (4).

Mutational events:

cer-p.37 (NGB 110921), *-p.43* (NGB 114379; GSHO 437), *-p.57* (NGB 110941) in Bonus (4, 5); *cer-p.77* (NGB 110961) in Bonus, *-p.252* (NGB 111139), *-p.259* (NGB 111146), *-p.300* (NGB 111187), *-p.339* (NGB 111226) in Foma (Clho 11333) (5, 12); *cer-p.522* (NGB 111410), *-p.573* (NGB 111461) in Foma, *-p.707* (NGB 111595) in Bonus (3); *cer-p.322* (NGB 111209) in Foma, *-p.777* (NGB 111665), *-p.795* (NGB 111683), *-p.874* (NGB 111762) in Bonus, *-p.1118* (NGB 112006), *-p.1142* (NGB 112030) in Kristina (NGB 1500) (6); *cer-p.631* (NGB 111519), *-p.646* (NGB 111534), *-p.888* (NGB 111776), *-p.889* (NGB 111777), *-p.905* (NGB 111793), *-p.972* (NGB 111860) in Bonus (7); *cer-p.939* (NGB 111827) in Bonus, *-p.1201* (NGB 112089), *-p.1206* (NGB 112094), *-p.1207* (NGB 112095), *-p.1210* (NGB 112098), *-p.1235* (NGB 112123) in Kristina (8); *cer-p.1292* (NGB 112180) in Kristina, *-p.1339* (NGB 112232), *-p.1344* (NGB 112232) in Bonus (9); *cer-p.1058* (NGB 111946) in Carlsberg II (Clho 10114), *-p.1383* (NGB 112271), *-p.1424* (NGB 112312) in Bonus (10); *cer-p.1442* (NGB 112330), *-p.1797* (NGB 117345) in Bonus (11).

Mutant used for description and seed stocks:

cer-p.43 in Bonus (GSHO 437, NGB 114379); *cer-p.37* (NGB 110921), *-p.43* (NGB 114379), and *-p.57* (NGB 110941) in Bonus are used for wax chemistry and wax structure studies (3, 12, 13); *cer-p.43* in Bowman (PI 483237)*5 (GSHO 2194), in Bowman*7 (BW120, NGB 20526).

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Prepared:

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Revised:

U. Lundqvist and J.D. Franckowiak, 1997. Barley Genet. Newsl. 26:360.

U. Lundqvist and J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:162-163.

BGS 412, Eceriferum-t, *cer-t*

Stock number: BGS 412
Locus name: Eceriferum-t
Locus symbol: *cer-t*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (4), except *Cer-t.977* (11).
Located in chromosome 5HL (2, 13); about 9.4 cM proximal from the *var1* (variegated 1) locus (2, 14, 15, 16); about 8.5 cM distal from the *cer-zp* (eceriferum-zp) locus (15, 16); *cer-t.22* is associated with SNP markers 2_0884 to 2_1077 (positions 210.59 to 223.57 cM) in 5H bin 11 of the Bowman backcross-derived line BW123 (1), in 5H bin 11.

Description:
Surface wax coating on the spike appears greatly reduced or absent (wax code +/- ++ ++ (4). Concerning the chemical epicuticular wax composition on the spike, the amount of the β -diketones and hydroxy- β -diketones is reduced and the alkan-2-ol containing esters are absent. The wax tubes are much shorter than in the wild type (17, 18). Plants of the Bowman backcross-derived line for *cer-t.22*, BW123, were similar to Bowman in agronomic traits, except plants were 10% shorter and grain yields were slightly lower (3).

Origin of mutant:
A gamma-ray induced mutant in Bonus (PI 189763) (4).

Mutational events:
cer-t.22 (NGB 110906, GSHO 441), *-t.46* (NGB 110938) in Bonus (4, 5); *cer-t.75* (NGB 110959), *-t.87* (NGB 110971) in Bonus, *-t.216* (NGB 111103), *-t.226* (NGB 111113), *-t.243* (NGB 111230), *-t.264* (NGB 111151), *-t.285* (NGB 111172), *-t.356* (NGB 111243), *-t.384* (NGB 111271), *-t.493* (NGB 111381) in Foma (Clho 11333) (5, 12); *cer-t.172* (NGB 111058), *-t.197* (NGB 111083), *-t.198* (NGB 111084), *-t.199* (NGB 111085) in Bonus, *-t.500* (NGB 111388), *-t.537* (NGB 111425), *-t.564* (NGB 111452) in Foma, *-t.657* (NGB 111545), *-t.664* (NGB 111552), *-t.671* (NGB 111559), *-t.719* (NGB 111607), *-t.726* (NGB 111614), *-t.738* (NGB 111626), *-t.743* (NGB 111631) in Bonus (5); *cer-t.617* (NGB 111505) in Foma, *-t.708* (NGB 111596), *-t.806* (NGB 111694), *-t.819* (NGB 111707), *-t.871* (NGB 111759) in Bonus, *-t.1088* (NGB 111976), *-t.1115* (NGB 112003) in Kristina (NGB 1500) (6); *cer-t.959* (NGB 111847), *-t.961* (NGB 111849) in Bonus, *-t.1176* (NGB 112064) in Kristina (7); *cer-t.625* (NGB 111513), *-t.641* (NGB 111529), *-t.933* (NGB 111821) in Bonus, *-t.1154* (NGB 112042), *-t.1171* (NGB 112059), *-t.1219* (NGB 112107), *-t.1244* (NGB 112132) in Kristina (8); *cer-t.1245* (NGB 112133) in Kristina (9); *cer-t.1360* (NGB 112248), *-t.1393* (NGB 112281), *-t.1401* (NGB 112289) in Bonus (10); *Cer-t.977* (NGB 111865), *-t.1710* (NGB 112523), *-t.1718* (NGB 112531) in Bonus (11).

Mutant used for description and seed stocks:
cer-t.22 in Bonus (GSHO 441, NGB 110906); *cer-t.46* in Bonus is used for wax chemistry and wax structure studies; *cer-t.22* in Bowman (PI 483237)*3 (GSHO 2119), in Bowman*7 (BW123, NGB 20529).

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Prepared:

U. Lundqvist and P. von Wettstein-Knowles. 1975. Barley Genet. Newsl. 5:130.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:363-364.

U. Lundqvist and J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:164-165.

BGS 415, Eceriferum-w, *cer-w*

Stock number: BGS 415
Locus name: Eceriferum-w
Locus symbol: *cer-w*

Previous nomenclature and gene symbolization:
None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 5HL (10); about 2.6 cM proximal from the *raw1* (smooth awn 1) locus (3, 11); but longer distances are reported (10); *cer-w.48* is associated with SNP markers 3_0098 to 2_0320 (positions 161.82 to 166.29 cM) in 5H bin 10 of the Bowman backcross-derived line BW125 (1), in 5H bin 10.

Description:

Surface wax coating on the spike appears greatly reduced or absent (wax code +/- ++ ++) (4, 9). Reduced surface wax coating occurs on the leaf sheath and the stem in the Bowman backcross-derived line (wax code - + ++) (2). Nodes lack surface wax and have a glossy appearance. Other morphological difference between the Bowman backcross-derived line with *cer-w.48*, BW125, and Bowman were not observed (2).

Origin of the mutant:

A gamma-ray induced mutant in Bonus (PI 189763) (4).

Mutational events:

cer-w.48 (NGB 110932, GSHO 1519) in Bonus (4, 5); *cer-w.280* (NGB 111167), *-w.347* (NGB 111234, GSHO 444), *-w.351* (NGB 111238), *-w.359* (NGB 111246), *-w.375* (NGB 111262), *-w.402* (NGB 111290) in Foma (Clho 11333) (5, 9); *cer-w.380* (NGB 111267), *-w.484* (NGB 111372), *-w.495* (NGB 111383), *-w.559* (NGB 111447), *-w.569* (NGB 111457), *-w.603* (NGB 111491), *-w.604* (NGB 111492) in Foma, *-w.691* (NGB 111579) in Bonus (5); *cer-w.771* (NGB 111659) in Bonus (6); *cer-w.858* (NGB 111746) in Bonus, *-w.1192* (NGB 112080) in Kristina (NGB 1500) (7); *cer-w.1445* (NGB 112333) in Bonus (8).

Mutant used for description and seed stocks:

cer-w.48 in Bonus (GSHO 1519, NGB 110932); *cer-w.48* in Bowman (PI 483237)*3 (GSHO 2122), in Bowman*7 (BW125, NGB 20531).

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1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
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Prepared:

U. Lundqvist. 1975. Barley Genet. Newsl. 5:133.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:367.

U. Lundqvist and J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:166-167.

BGS 427, Eceriferum-zi, *cer-zi*

Stock number: BGS 427
Locus name: Eceriferum-zi
Locus symbol: *cer-zi*

Previous nomenclature and gene symbolization:
None.

Inheritance:

Monofactorial recessive (11).

Located in chromosome 1HL (12); about 1.3 cM proximal from the *cer-e* (eceriferum-e) locus (3, 12), about 16.1 cM proximal from the *nec1* (necrotic leaf spot 1) locus (3, 4), *cer-zi.68* is associated with SNP markers 1_0744 to 2_1361 (positions 39.84 to 82.35 cM) in 1H bins 05 to 08 of the Bowman backcross-derived line BW165 (1), likely in 1H bin 08.

Description:

Surface wax coating on the spike, leaf sheath, and stem is reduced somewhat (wax code + + ++) (11). No agronomic differences between plants of the Bowman backcross-derived line for *cer-zi.68*, BW165, and Bowman plants were observed (2).

Origin of mutant:

An ethylene imine induced mutant in Bonus (PI 189763) (11).

Mutational events:

cer-zi.68 (NGB 110952, GSHO 456) in Bonus, *-zi.219* (NGB 111106), *-zi.409* (NGB 111297), *-zi.410* (NGB 111298) in Foma (Clho 11333) (5, 11); *cer-zi.138* (NGB 111023), *-zi.674* (NGB 111562), *-zi.701* (NGB 111589) in Bonus (5); *cer-zi.815* (NGB 111703), *-zi.846* (NGB 111734), *-zi.971* (NGB 111859) in Bonus (6); *cer-zi.1104* (NGB 111992), *-zi.1119* (NGB 112007), *-zi.1145* (NGB 112033) in Kristina (NGB 1500) (7); *cer-zi.1314* (NGB 112202) in Kristina (8); *cer-zi.979* (NGB 111867) in Bonus (9); *cer-zi.633* (NGB 111521), *-zi.1414* (NGB 112302), *-zi.1465* (NGB 112353) in Bonus (10).

Mutant used for description and seed stocks:

cer-zi.68 in Bonus (GSHO 456, NGB 110952); *cer-zi.68* in Bowman (PI 483237)*6 (GSHO 2047), in Bowman *8 (BW165, NGB 21997).

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Prepared:

U. Lundqvist. 1975. Barley Genet. Newsl. 5:145.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:378.

U. Lundqvist and J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:168-169.

BGS 438, Eceriferum-zu, *cer-zu*

Stock number: BGS 438
Locus name: Eceriferum-zu
Locus symbol: *cer-zu*

Previous nomenclature and symbolization:
None.

Inheritance:
Monofactorial recessive 4).
Located in chromosome 1HS (1); *cer-zu.122* is associated with SNP markers 1_0764 to 2_0095 (positions 61.55 to 89.85 cM) in 1H bins 06 to 08 of the Bowman backcrossed-derived line BW176 (1).

Description:
Surface wax coating on the spike appears absent, the wax coating on the leaf sheath and stem is reduced (wax code - + ++) (4). Leaf blades become golden yellow at or shortly after heading and later necrotic spots develop on the upper surface of the leaf blade (3). The necrosis is observed in crosses to Bowman, but is not retained in the backcross-derived line for *cer-zu.122*, BW176. Plants of the BW176 line were morphological and agronomically similar to Bowman in trials (2).

Origin of mutant:
An ethyl methanesulfonate induced mutant in Bonus (PI 189763) (3).

Mutational events:
cer-zu.122 (NGB 111007, GSHO 1528) in Bonus (4); *cer-zu.973* (NGB 111861) in Bonus (5); *cer-zu.1163* (NGB 112051) in Kristina (NGB 1500), *-zu.1419* (NGB 112307), *-zu.1428* (NGB 112316), *-zu.1447* (NGB 112325); *-zu.1494* (NGB 112382) in Bonus (6); , *cer-zu.1570* (NGB 112458), *-zu.1571* (NGB 112459) in Nordal, *cer-zu.1762* (NGB 112577), *-zu.1784* (NGB 112599) in Bonus (7).

Mutant used for description and seed stocks:
cer-zu.122 in Bonus (GSHO 1528, NGB 111007); *cer-zu.122* in Bowman (PI 483237)*5 (GSHO 2206, BW176, NGB 22008).

References:
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Prepared:
U. Lundqvist. 1975. *Barley Genet. Newsl.* 5:156.

Revised:
U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:390.
U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:170.

BGS 445, Eceriferum-yb, *cer-yb*

Stock number: BGS 445
Locus name: Eceriferum-yb
Locus symbol: *cer-yb*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (5).
Located in chromosome 2HL (3); near the *Gth1* (toothed lemma 1) locus based on linkage drag (3); *cer-yb.200* is associated with SNP markers 2_0647 to 1)1533 (positions 85.71 to 141.56 cM) in 2H bins 07 to 10 of the Bowman backcross-derived line BW133 (1), likely in 2H bin 09.

Description:
Surface wax coating on the leaf blade appears absent (wax code ++ ++ -) (5). Plants of the Bowman backcross-derived line with *cer-yb.200*, BW133, headed 2 to 3 days later than Bowman and had 4 to 5 more kernels per spike. Other morphological traits of BW133 were similar to those of Bowman (2).

Origin of mutant:
A neutron induced mutant in Bonus (PI 189763) (4).

Mutational events:
cer-yb.200 (NGB 111086, GSHO 1535) in Bonus, *-yb.316*, (NGB 111203), *-yb.453* (NGB 111341) in Foma (CIho 11333) (5); *cer-yb.1174* (NGB 112062) in Kristina (NGB 1500) (6); *cer-yb.1211* (NGB 112099) in Kristina (7).

Mutant used for description and seed stocks:
cer-yb.200 in Bonus (GSHO 1535, NGB 111086); *cer-yb.200* in Bowman (PI 483237)*6 (GSHO 1896), in Bowman*7 (BW133, NGB 20539).

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Prepared:
U. Lundqvist. 1975. *Barley Genet. Newsl.* 5:163.

Revised:
U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:397.
J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:171.

BGS 446, Eceriferum-yc, *cer-yc*

Stock number: BGS 446
Locus name: Eceriferum-yc
Locus symbol: *cer-yc*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (4).
Location in chromosome 6H or 7HS (1); *cer-yc.135* is associated with SNP markers 1_0061 to 1_1261 (positions 70.15 to 107.26 cM) in 6H bins 05 to 07 and SNP markers 2_1419 to 1_0838 (positions 0.0 to 49.53 cM) in 7H bins 01 to 04 of the Bowman backcross-derived line BW134 (1).

Description:
Surface wax coating on the spike appears absent (wax code - ++ ++) (3). Surface wax on the leaf sheath appears reduced in the Bowman backcross-derived line (wax code - + ++). The long-chain *n*-alkanes on the spike were reduced without greatly altering the chain-length distributions of the minor hydrocarbons (7). Compared to Bowman, the Bowman backcross-derived line for *cer-yc.135*, BW134, had kernels that were slightly smaller with weights about 10% less. Grain yields for BW134 were about 3/4 those for Bowman. Other morphological differs from Bowman were not observed (2).

Origin of mutant:
An ethylene imine mutant in Bonus (PI 189763) (2).

Mutational events:
cer-yc.135 (NGB 111020, GSHO 1536) in Bonus (4); *cer-yc.523* (NGB 111411) in Foma (CIho 11333) (5); *cer-yc.438* (NGB 111326), *-yc.439* (NGB 111327) in Foma, *-yc.783* (NGB 111671 in Bonus (6).

Mutant used for description and seed stocks:
cer-yc.135 in Bonus (GSHO 1536, NGB 111020); *cer-yc.135* in Bowman (PI 483237)*3 (GSHO 2211), in Bowman*5 (BW134, NGB 20540).

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Prepared:
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Revised:
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U. Lundqvist and J. D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:172.

BGS 465, Male sterile genetic 28, *msg28*

Stock number: BGS 465
Locus name: Male sterile genetic 28
Locus symbol: *msg28*

Previous nomenclature and gene symbolization:

Male sterile as = *msg*,as (3).

Inheritance:

Monofactorial recessive (3, 6).

Located in chromosome 2HS (1); associated with SNP markers 2_1015 to 2_0864 (positions 48.68 to 55.52 cM) in 2HS bin 05 of a plant presumed to be a heterozygote from the Bowman backcross-derived line BW563 (1); Previously located in chromosome 6H, near the *rob1* (orange lemma 1) locus (2).

Description:

Selfing - none (3).

Outcrossing - complete female fertility (3, 6).

Stamens - anthers rudimentary, with no stomium or filament elongation (6).

Pollen - non-staining, shrunken, and no normal-appearing grains (6).

Cytology - normal meiosis (6).

Origin of mutant:

A spontaneous mutant in York (CIho 10075) (6).

Mutational events:

msg28.as (GSHO 2380) in York (MSS311) (4, 5, 6).

Mutant used for description and seed stocks:

msg28.as in York (GSHO 2380); *msg28.as* in Bowman (PI 483237)*7 (GSHO 2079, BW563).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
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Prepared:

E.A. Hockett. 1986. *Barley Genet. Newsl.* 16:48.

Revised:

E.A. Hockett. 1991. *Barley Genet. Newsl.* 20:95.

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:412.

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:173.

BGS 475, Laxatum-c, *lax-c*

Stock number: BGS 475
Locus name: Laxatum-c
Locus symbol: *lax-c*

Previous nomenclature and gene symbolization:

Laxatum-21 = *lax-21* (3, 4, 5).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 6HL (6); over 27.3 cM distal from the *lax-b* (laxatum-b) locus (6); *lax-c.21* is associated with SNP markers 1_0015 to 2_0733 (positions 160.38 to 180.69 cM) in 6H bins 10 to 11 of the Bowman backcross-derived line BW460 (1).

Description:

The grain is thin and angular and caryopses are exposed between the lemma and palea. The awn has a very wide base. Rachis internodes are about 7% longer than normal. In the original Bonus stock, the tip of the spike is frequently sterile, and the tiller number is reduced (4). Plants of the Bowman backcross-derived line for *lax-c.21*, BW460, were 3/4 the height of Bowman. Rachis internodes of BW460 plants were slightly longer in some trials. The awns and peduncle were slightly shorter than small part of the Bowman plants. Kernels were about 10% shorter and thinner and their weights were about 20% lighter, 4.8 mg vs. 5.7 mg, than those of Bowman. Grain yields were about 3/4 those of Bowman (2). Plants of the Bowman backcross-derived line for *lax-c.231* (*sld.l*), BW858, were similar to those of BW460, except they had more pronounced spiral coiling of the neck and occasionally formed small branches on the awn (2).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (4).

Mutational events:

lax-c.21 (NGB 116355, GSHO 1777), -c.23 (NGB 116358) in Bonus (4, 5); *lax.231* (*sld.l*, NGB 116459, GSHO 2478) in Foma (CIho 11333) may be an allele based on phenotype and SNP markers retained in 6HL of its Bowman backcross derived line, BW858, NGB 22295) (1, 2).

Mutant used for description and seed stocks:

lax-c.21 in Bonus (GSHO 1777, NGB 116355); *lax-c.21* in Bowman (PI 483237)*6 (GSHO 2086), in Bowman*7 (BW460, NGB 20691); *lax-c.231* (*sld.l*) in Bowman*3 (GSHO 2359), in Bowman*6 (BW858, NGB 22295).

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1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
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4. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. *Hereditas* 103:239-253.
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Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. *Barley Genet. Newsl.* 16:58.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:423.

U. Lundqvist and J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:174-175.

BGS 518, Semidwarf 1, *sdw1*

Stock number: BGS 518
Locus name: Semidwarf 1
Locus symbol: *sdw1*

Previous nomenclature and gene symbolization:

Denso dwarf = *denso* (7, 17).

Hordeum vulgare gibberellin 20-oxidase = *Hv20ox2* (9, 10).

Inheritance:

Monofactorial recessive (7, 18); some F₁'s are intermediate in height (1, 12).

Location in chromosome 3HL (2, 13); probably proximal from the *gsh2* (glossy sheath 2) locus and near RFLP marker PSR170 (13); in bin 3H-11 (11); near RFLP marker R1545 (21); *sdw1* is close to SNP marker 1_0867 (14); *sdw1.a* is associated with SNP markers 1_0044 to 2_0650 (positions about 190 to 192.00 cM) in 3H bin 12 of the Bowman backcross-derived line BW827 (4); *sdw1.d* is associated with SNP markers 2_0023 to 1_0821 (positions 169.94 to 190.87 cM) in 3H bins 11 and 12 of the Bowman backcross-derived line BW828 (4), in 3H bin 12.

Description:

Plants homozygous for the *sdw1.a* gene ranged from 10 to 30 cm shorter than normal sibs, with expression partial dependent on environment (1, 17, 19). Spike length was variable, but fully as long as normal barley. The stock used for description of the *sdw1.a* gene, M21, has the short straw and long spike of the original 'Jotun Mutant' as well as a large culm diameter from its parent 'Vantage' (1, 19). The semidwarf mutants, 'Diamant' and 'Abed Denso', are alleles at the *sdw1* locus (7, 15). Alleles at the *sdw1* locus are associated with semi-prostrate juvenile growth (7, 17), delayed maturity (5, 7, 8, 17, 20), smaller grain size (7), and reduced malt quality (5, 8, 17). The *sdw1* mutants are GA sensitive (3, 21). They are very likely mutants in an orthologue of the rice *sd1* gene (21), which encodes a GA-oxidase that produces lower levels of GA and reduced levels of cause the dwarf phenotype (9, 16). A gibberellin 20-oxidase gene (*Hv20ox2*) was identified as the candidate gene for *sdw1* (9, 10). The reduced expression of *Hv20ox2* increased the number of effective tillers and enhanced grain yield (10). The reduction in *Hv20ox2* levels was 4-fold in the *sdw1.d* mutant and 60-fold in the *sdw1.a* mutant (10). Plants of the Bowman backcross-derived line for *sdw1.a*, BW827, were 15 to 30% shorter than Bowman and heading was delayed 1 to 3 days. Plants of the Bowman backcross-derived line for *sdw1.d*, BW828, were 10 to 20% shorter than Bowman, heading was delayed 1 to 3 days, and spikes had 1 to 2 more kernels in some traits. Kernels of BW827 and BW828 were up to 10% lighter than Bowman kernels in some trials. Grain yields of BW828 were similar to those of Bowman, while those of BW827 were about 85% of the Bowman yields (6).

Origin of mutant:

An X-ray induced mutant in the Norwegian cultivar Jotun (PI 467357) isolated as Jotun 22 by Knut Mikaelsen (1, 12).

Mutational events:

sdw1.a (66/86, GSHO 1414) in Jotun (19); *sdw1.c* (*denso*) in Abed Denso (PI 361639) (7); *sdw1.d* (Diamant, PI 330397, PI 467775) in Valticky (PI 268173) (7); *sdw1.e* (Risø no. 9265) in Bomi (PI 43371) (7). Note that the *denso* name was original assigned to the *sdw1.c* mutant (7), but now cultivars with the *sdw1.d* mutant from Diamant are described as having the *denso* mutant.

Mutant used for description and seed stocks:

sdw1.a in M21 (Clho 15481, GSHO 2513) from the cross Jotun Mutant/Kindred//Vantage (19); *sdw1.d* in Trumpf (Triumph, PI 548762, GSHO 2465) from Diamant; *sdw1.a* from a Jotun derivative in Bowman (PI 483237)*7 (GSHO 1978), in Bowman*8 (BW827, NGB 22264); *sdw1.d* from Trumpf in Bowman*4 (GSHO 1979), in Bowman*5 (BW828, NGB 22265).

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Prepared:

D.C. Rasmusson. 1988. *Barley Genet. Newsl.* 18:87 as BGS 468.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:444-445.

J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:277-278.

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:176-178.

BGS 521, Mottled leaf 1, *mtt1*

Stock number: BGS 521
Locus name: Mottled leaf 1
Locus symbol: *mtt1*

Previous nomenclature and gene symbolization:

Mottled leaves = *mt* (5).

Mottled leaves 3 = *mt*₃ (4).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 1H (4); based on linkage drag near the *s/s1.a* (small lateral spikelet 1) locus (3); *mtt1.a* is associated with SNP markers 1_0760 to 2_0229 (positions 52.84 to 106.61 cM) in 1H bins 05 to 10 of the Bowman backcross-derived line BW600 (1), likely in 1H bin 08.

Description:

Seedlings have two to four clearly marked white bands across or partially across the leaves. Necrosis of the white region occurs later and the leaf is constricted in these regions. Temperatures at germination over 20°C reduce the extent of mottling. Plant mortality is low at Edmonton, Alberta, Canada, where temperatures are low, but nearly 100% at St. Paul, Minnesota, USA (4). Heading of the Bowman backcross-derived line BW600 was delayed by about 6 days, plants were approximately 10% shorter, and grain yields were 15 to 30% of normal. Compared to Bowman, kernels of BW600 were slightly shorter and narrower and kernel weights were 10 to 30% lower (2).

Origin of mutant:

An induced mutant in Montcalm (Clho 7149) (4).

Mutational events:

mtt1.a (*mt*) in Montcalm (Alb Acc 284, OUM070, GSHO 622) (4).

Mutant used for description and seed stocks:

mtt1.a in Montcalm (OUM070, GSHO 622); *mtt1.a* in Bowman (PI 483237)*4 (GSHO 2036), in Bowman*7 (BW600, NGB 22166).

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Prepared:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:448.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:179.

BGS 522, Eceriferum-yi, *cer-yi*

Stock number: BGS 522
Locus name: Eceriferum-yi
Locus symbol: *cer-yi*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (4).
Located in chromosome 2H (1); *cer-yi.254* is associated with SNP markers 1_0326 to 1_1533 (positions 16.91 to 141.56 cM) in 2H bins 01 to 10 of the Bowman backcross-derived line BW140 (1).

Description:
Surface wax coating on the leaf blade appears absent (wax code ++ ++ -) (4). Plants of line Bowman backcross-derived line containing *cer-yi.254*, BW140, headed over one day later than Bowman, had 2 or 3 more kernels per spike, and kernels were slightly shorter and lighter. Grain yields were slightly lower than those of Bowman (2). During development of the line BW140, slightly reduced fertility was observed in F1 plants (2). Since the SNP markers retained BW140 involve a large portion of 2HL (1), the *cer-yi.254* mutant may include an inversion (1, 2).

Origin of mutant:
An X-ray induced mutant in Foma (Clho 11333) (3).

Mutational events:
cer-yi.254 (NGB 111141, GSHO 1542) in Foma, *-yi.956* (NGB 111844) in Bonus (PI 189763) (4); *cer-yi.1213* (NGB 112101) in Kristina (NGB 1500), *-yi.1353* (NGB 112241) in Bonus (5).

Mutant used for description and seed stocks:
cer-yi.254 in Foma (GSHO 1542, NGB 111141); *cer-yi.254* in Bowman (PI 483237)*3 (GSHO 2213), in Bowman*4 (BW140, NGB 20546).

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1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
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Prepared:
U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:449.

Revised:
U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:180.

BGS 545, Intermedium spike-i, *int-i*

Stock number: BGS 545
Locus name: Intermedium spike-i
Locus symbol: *int-i*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (3).
Location is chromosome 2HS (1), *int-i.39* is associated with SNP markers 1_1110 to 2_1304 (positions to 34.31 to 58.56 cM) in 2H bins 04 and 05 of the Bowman backcross-derived line BW426) (1), likely in 2H bin 04 or 05.

Description:
Lateral spikelets are enlarged and slightly pointed at the apex, but they fail to set seed. The tip of the spike may have very short rachis internodes and appears very dense or fasciated (4). Plants of the Bowman backcross-derived line BW426 exhibited elongation of the basal rachis internode. BW426 plants were about 3/4 the height of Bowman plants and the spikes had slightly long rachis internodes. Although kernels per spike and seed weights were variable over nurseries, BW426 plants had in general fewer kernels/spike and kernel weights were 10 to 15% below those of Bowman. Grain yields of BW426 were 1/2 to 3/4 of normal (2).

Origin of mutant:
An ethylene imine induced mutant in Kristina (NGB 1500) (4).

Mutational events:
int-i.39 (NGB 115457, GSHO 1769) in Kristina (3, 4).

Mutant used for description and seed stocks:
int-i.39 in Kristina (GSHO 1769, NGB 115457); *int-i.39* in Bowman (PI 483237)*4 (GSHO 2272), in Bowman*6 (BW426, NGB 20659).

References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
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Prepared:
U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:471.

Revised:
J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:181.

BGS 551, Breviaristatum-f, *ari-f*

Stock number: BGS 551
Locus name: Breviaristatum-f
Locus symbol: *ari-f*

Previous nomenclature and gene symbolization:

Breviaristatum-21 = *ari-21* (3, 4).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 7H (1); *ari-f.21* is associated with SNP markers 1_0721 to 1_1343 (positions 82.82 to 134.43 cM) in 7H bins 06 to 08 of the Bowman backcross-derived line BW044 (1).

Description:

Awns are thin and often 1/2 to 3/4 normal length, and awn length decreases toward the top of the spike. Spikes are more lax and have fewer rachis internodes than those of parental cultivars. Deformation of the lemma apex causes apical kernels to be naked (4). Plants of the Bowman backcross-derived line for *ari-f.21*, BW044, were 15 to 25% shorter than Bowman and had awns that extended 4 cm beyond the tip of the spike vs. 11 to 12 cm for Bowman. Kernels of BW044 were shorter, 8.6 vs. 9.6 mm, and thinner, 3.3 vs. 3.8 mm, than those of Bowman and weighed 40% less, 3.5 vs. 5.8 mg. The grain yields of BW044 ranged from very little to 20% those of Bowman (2).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (2).

Mutational events:

ari-f.21 (NGB 115869, GSHO 1654), in Bonus (5); *ari-f.42* (NGB 115893), *-f.47* (NGB 115899) in Bonus (4); *ari-f.52* (NGB 115905), *-f.54* (NGB 115907), *-f.55a* (NGB 115908) in Bonus (5); *ari-f.113* (NGB 115925) in Foma (Clho 11333) (4); *ari-f.115* (NGB 115927) in Foma (5); *ari-f.123* (NGB 115935), *-f.136* (NGB 115946) in Foma (4); *ari-f.155* (NGB 115964) in Foma (5); *ari-f.168* (NGB 115978), *-f.169* (NGB 115979), *-f.170* (NGB 115980), *-f.224* (NGB 116033), *-f.225* (NGB 116034), *-f.233* (NGB 116043), *-f.235* (NGB 116045) in Foma, *-f.253* (NGB 116064), *-f.254* (NGB 116062), *-f.260* (NGB 116069), *-f.266* (NGB 116076) in Kristina (NGB 1500) (4); *ari-f.268* (NGB 116079), *-f.275* (NGB 116087), *-f.294* (NGB 116114), *-f.295* (NGB 116115), *-f.300* (NGB 116123) in Kristina (5).

Mutant used for description and seed stocks:

ari-f.21 in Bonus (GSHO 1654, NGB 115869); *ari-f.21* in Bowman (PI 483237)*5 (GSHO 2158), in Bowman*7 (BW044, NGB 20452).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:477.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:182-183.

BGS 554, Breviaristatum-m, *ari-m*

Stock number: BGS 554
Locus name: Breviaristatum-m
Locus symbol: *ari-m*

Previous nomenclature and gene symbolization:

Breviaristatum-28 = *ari-28* (4).

Inheritance:

Monofactorial recessive (4).

Location in chromosome 7HS (1); *ari-m.28* is associated with SNP markers 2_0710 to 2_0307 (positions 4.74 to 9.55 cM) in 7H bin 01 of the Bowman backcrossed-derived line BW051 (1), in 7H bin 01.

Description:

Plants are semidwarf (2/3 normal height) and can be placed in the brachytic class of semidwarfs (3). Kernels are globe-shaped and awns are about 1/2 normal length (4). Spikes are slightly more lax than normal. Based on the chromosomal position of retained SNP markers and morphological characteristics of Bowman backcross-derived line BW051, the *ari-m.28* might be an allele at the *brh1* (brachytic 1) locus (1, 2).

Origin of mutant:

A gamma-ray induced mutant in Bonus (PI 189763) (4).

Mutational events:

ari-m.12 (NGB 115858), *-m.28* (GSHO 1661, NGB 115876) in Bonus, *-m.141* (NGB 115951), *-m.177* (NGB 115987) in Foma (Clho 11333), *-m.251* (NGB 116059) in Kristina (NGB 1500) (4); *ari-m.269* (NGB 116081) in Kristina (NGB 1500) (4, 5).

Mutant used for description and seed stocks:

ari-m.28 in Bonus (GSHO 1661, NGB 115876); *ari-m.28* in Bowman (PI 483237)*6 (GSHO 2161), in Bowman*8 (BW051, NGB 20459).

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:480.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:184.

BGS 555, Breviaristatum-n, *ari-n*

Stock number: BGS 555
Locus name: Breviaristatum-n
Locus symbol: *ari-n*

Previous nomenclature and gene symbolization:

Breviaristatum-45 = *ari-45* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 7H (1); *ari-n.45* is associated with SNP markers 1_0721 to 1_0700 (positions 82.82 to 144.00 cM) in 7H bins 06 to 08 of the Bowman backcrossed-derived line BW052 (1).

Description:

Awns are 3/4 normal length and arise at an oblique angle, and they are drastically shortened towards the top of the spike (3). Plant height is normal, but spikes are short due to a reduced number of rachis internodes and apical abortion (3). Plants of the Bowman backcross-derived line for *ari-n.45*, BW052, varied in height over environments from 20% shorter to equal to Bowman. Awns extended in specific environments from 2 to 6 cm beyond the tip of the spike while those of Bowman extended about 11 cm. The kernels of BW052 were thinner, 3.5 vs. 3.8 mm, than those of Bowman, slightly shorter and about 25% less, 4.4 vs. 5.9 mg. Grain yields of BW052 varied from 2/3 to 3/4 those of Bowman (2).

Origin of mutant:

A gamma-ray induced mutant in Bonus (PI 189763) (3).

Mutational events:

ari-n.45 (NGB 115897, GSHO 1662), *-n.46* (NGB 115898) in Bonus, *-n.147* (NGB 115958), *-n.163* (NGB 115973), *-n.164* (NGB 115974), *-n.181* (NGB 115991), *-n.219* (NGB 116028), *-n.220* (NGB 116029), *-n.231* (NGB 116041) in Foma (CIho 11333), *-n.258* (NGB 116067), *-n.292* (NGB 116112) in Kristina (NGB 1500) (3, 4).

Mutant used for description and seed stocks:

ari-n.45 in Bonus (GSHO 1662, NGB 115897); *ari-n.45* in Bowman*6 (BW052, NGB 20460).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
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3. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of breviaristatum mutants in barley. *Hereditas* 80:263-278.
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Prepared:

U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:481.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:185.

BGS 556, Breviaristatum-o, *ari-o*

Stock number: BGS 556
Locus name: Breviaristatum-o
Locus symbol: *ari-o*

Previous nomenclature and gene symbolization:

Breviaristatum-40 = *ari-40* (4).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 7HL (1); *ari-o.40* is associated with SNP markers 1_0547 and 3_0166 (about position 232 cM) in 7H bin 14 of the Bowman backcross-derived line BW053 (1).

Description:

Plants are semidwarf (2/3 normal height) and can be placed in the brachytic class of semidwarfs (3). The culm may have a short or extra internode and a leafy bract below the spike. The peduncle is often slightly coiled, and the basal rachis internode is elongated. Kernels are globe-shaped, and awns are about 3/4 normal length (4). Plants of BW053, the Bowman backcross-derived line for mutant *ari-o.40*, were about 25% shorter than Bowman, 65 vs. 90 cm, and awns were about 3 cm shorter. Rachis internode lengths and kernels were slightly shorter for BW053, but spikes had 2 to 3 more kernels. Kernels of BW053 were slightly shorter than those of Bowman. Kernel weights varied from slightly more to 20% less. Grain yields for BW053 varied from 20 to 50% of the Bowman yields (2).

Origin of mutant:

An ethylene imine induced mutant in Bonus (PI 189763) (4).

Mutational events:

ari-o.40 (NGB 115890, GSHO 1663), -o.43 (NGB 115894), in Bonus (4); *ari-o.143* (NGB 115953), in Foma (CIho 11333), -o.297 (NGB 116116), -o.301 (NGB 116124), -o.304 (NGB 116129), -o.306 (NGB 116133) in Kristina (NGB 1500) (5).

Mutant used for description and seed stocks:

ari-o.40 in Bonus (GSHO 1663, NGB 115890); *ari-o.40* in Bowman (PI 483237)*6 (GSHO 2162), in Bowman*7 (BW053, NGB 20461).

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:482.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:186.

BGS 559, Breviaristatum-r, *ari-r*

Stock number: BGS 559
Locus name: Breviaristatum-r
Locus symbol: *ari-r*

Previous nomenclature and gene symbolization:

Breviaristatum-14 = *ari-14* (4).

Inheritance:

Monofactorial recessive (4).

Location in chromosome 5H (1); *ari-r.14* is associated with SNP markers 1_1198 to 2_1275 (positions 73.70 to 104.73 cM) in 5H bins 04 to 06 of the Bowman backcross-derived line BW056 (1).

Description:

Plants are semidwarf (less than 1/2 normal height) with compact spikes and globe-shaped kernels. Awns are stiff and less than 1/3 normal length (4). Plants are vigorous, but heading is delayed. This mutant can be placed in the brachytic class of semidwarfs based on growth pattern (3). The growth habit of *ari-r.14* is semi-prostrate. Plants of the Bowman backcross-derived line for *ari-r.14* (BW056) were 1/3 to 1/2 the height of Bowman with peduncles about 1/2 normal length. Leaf blades were short, about half normal, but width was near normal. Awns were 1/2 to 3/4 normal length, the number of fertile spikelets per spike was reduced by about 20%, and spikes had shortened rachis internodes, 3.3 vs. 4.5 mm. Kernels of BW056 were 25% shorter than those of Bowman and kernel weights were nearly 40% less, 3.3 vs. 5.6 mg. Grain yield of BW056 were about 1/3 those of Bowman (2).

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763) (4).

Mutational events:

ari-r.14 (GSHO 1666, NGB 115860) in Bonus, *-r.202* (NGB 116011) in Foma (Clho 11333) (4); *ari-r.236* (NGB 116046) in Foma (5); *ari-r.282* (NGB 116098) in Kristina (NGB 1500) (4); *ari-r.314* (NGB 116145), *-r.318* (NGB 116151) in Kristina (5).

Mutant used for description and seed stocks:

ari-r.14 in Bonus (GSHO 1666, NGB 115860); *ari-r.14* in Bowman (PI 483237)*6 (GSHO 2165, BW056, NGB 20464).

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:485.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:187.

BGS 567, Erectoides, *ert-v*

Stock number: BGS 567
Locus name: Erectoides-v
Locus symbol: *ert-v*

Previous nomenclature and gene symbolization:

Erectoides-57 = *ert-57* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 6H (1); *ert-v.57* is associated with SNP markers 1_0061 to 1_1261 (positions 70.15 to 107.26 cM) in 6H bins 05 to 07 of the Bowman backcross-derived line BW326 (1).

Description:

Spikes appear abnormal with irregular placement of kernels. Rachis internode length is reduced with average values from 1.7 to 3.1 mm. Plants are weak and semi-sterile, anthers are often whitish, and culm length is about 3/4 of normal (4). Phenotypically the *ert-v.57* mutant could be classified as an opposite spikelet type. Plants of the Bowman backcross-derived line for *ert-v.57*, BW326, have relatively low vigor with grain yield about 1/3 those of Bowman. BW326 headed 3 days later than Bowman, was 15 to 20% shorter, and had 3 to 6 fewer kernels per spike. Rachis internode lengths averaged 3.2 vs. 4.6 mm for Bowman. Kernel weights for BW326 were 20 to 25% lower and test weights were very low (2).

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763) (3).

Mutational events:

ert-v.57 (NGB 112656, GSHO 497) in Bonus (3); *ert-v.172* (NGB 112772) in Bonus, -
v.313 in Foma (CIho 11333) (4).

Mutant used for description and seed stocks:

ert-v.57 in Bonus (GSHO 497, NGB??); *ert-v.57* in Bowman (PI 483237)*6 (GSHO 2258), in Bowman*7 (BW326, NGB 22121).

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:493.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:188.

BGS 595, Anthocyanin-deficient 4, *ant4*

Stock number: BGS 595
Locus name: Anthocyanin-deficient 4
Locus symbol: *ant4*

Previous nomenclature and symbolization:

Exrubrum = rub (3, 4).

Inheritance:

Monofactorial recessive (6, 7).

Located in chromosome 4H (1), *ant4.16* is associated with SNP markers 2_1122 to 1_1500 (positions 47.7 to 115.92 cM) in 4H bins 05 to 08 of the Bowman backcross-derived line BW024 and also SNP markers 2_0972 to 1_0139 (positions 156.09 to 160.38 cM) in 6H bin 09 of BW024 (1).

Description:

Depending on the growing conditions, a slight pigmentation can be observed in the auricles, awns and lemmas of the mutant plants. The amount of anthocyanin pigmentation was clearly decreased compared to the mother cultivar (5, 7). The original mutant alleles, *ant4.16* and *ant4.17*, were taller and later maturing than their mother cultivar Foma (5, 7). The Bowman backcrossed derived line for *ant4.16* (BW024) was 10 to 20% taller than Bowman in both field and greenhouse tests, partially because its peduncles were longer (2). Slightly earlier heading of BW024 was observed under glasshouse conditions. BW024 plants lodged more than Bowman in field tests. The spikes of BW024 had one to three fewer kernels and rachis internodes were slightly shorter. Kernels were 10 to 15% lighter and grain yields were slightly lower than those of Bowman (2).

Origin of mutant:

An ethylene imine induced mutant in Foma (CIho 11333) (5).

Mutational events:

ant4.11 (NGB 114560), *4.16* (NGB 114565, GSHO 1642), *4.17* (NGB 114566), *4.28* (NGB 114583), *4.31* (NGB 114586) in Foma (7); *ant4.32* (NGB 114587) in Foma (5); *ant4.37* (NGB 114592) in Foma (7); *ant4.40* (NGB 114595) in Bonus (PI 189763) (7); *ant4.44* (NGB 119349) in Bonus (6); *ant4.53* (NGB 111870) in Bonus (5); *ant4.124* in Nordal (NGB 13680) (5).

Mutant used for description and seed stock:

ant4.11 in Foma (NGB 114560); *ant 4.16* in Foma (NGB 114565, GSHO 1642); *ant4.16* in Bowman (PI 483237)*3 (GSHO 2267), in Bowman*7 (BW024, NGB 20432).

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Prepared:

B. Jende-Strid. 1999. *Barley Genet. Newsl.* 29:83.

Revised:

J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:189-190.

BGS 604, Proanthocyanidin-free 22, *ant22*

Stock number: BGS 604
Locus name: Proanthocyanidin-free 22
Locus symbol: *ant22*

Previous nomenclature and symbolization:
None.

Inheritance:

Monofactorial recessive (5, 6).

Located in chromosome 2HL (2); closely linked to the *Zeo2* (Zeocriton 2) locus (2); *ant22.1508* is associated with SNP markers 1_1340 to 2_0895 (positions 166.06 to 209.87 cM) in 2H of the Bowman backcross-derived line BW022 (1). Previously located in 7H when the dense spike trait was believed to be controlled by the *dsp1* (dense spike 1) gene (2), likely in 2HL bin 13 based on the lack of recombination with the dense spike trait (*Zeo2*); previously located in chromosome 7H (1, 3).

Description:

No anthocyanin pigmentation is observed in the vegetative parts of the mutant plants. The testa layers of the grains of the *ant22* mutants lack proanthocyanidins and catechins but accumulate homoeriodictyol and chrysoeriol (7, 8). It is likely that the *ant22* gene codes for one subunit and the *ant17* gene for the other subunit of the dimeric flavanone 3-hydroxylase enzyme, which catalyzes the conversion of flavanones into dihydroflavonols (7, 9). Plants of the Bowman backcross-derived line BW022 were slightly shorter than Bowman and shorter rachis internodes, 2.8 vs. 4.6 mm. The kernels of BW022 plants were 5 to 10% lighter and slightly shorter and thinner. The reduced in grain size appear to be an effect of the *ant22.1508* allele in BW022 while reductions in culm length and rachis internode length appeared associated with the *Zeo2* allele (3). A close linkage of the *ant22.1508* allele to the short rachis internode trait was observed in BW022 (3). But instead of *dsp1* (dense spike 1) in 7H, the critical dense spike trait was shown to be in 2HL where the *Zeo2* gene is located (2).

Origin of mutant:

A sodium azide induced mutant in Hege 802 (4).

Mutational events:

ant22.212 in Hege 802 (4); *ant22.603* in Harrington (CN 37389) (6); *ant22.1500*, *22.1501*, *22.1504* in Amagi-Nijo (4); *ant22.1508* (NGB 13705, GSHO 1635) in Haruna-Nijo (5).

Mutant used for description and seed stock:

ant22.1508 in Haruna-Nijo (NGB 13705, GSHO 1635); *ant22.1508* in Bowman (PI 483237)*3 (GSHO 1841), in Bowman*6 (BW022, NGB 20430).

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Prepared:

B. Jende-Strid. 1999. *Barley Genet. Newsl.* 29:95.

Revised:

J.D. Franckowiak 2011. *Barley Genet. Newsl.* 41:191-192.

BGS 614, Zeocriton 2, Zeo2

Stock number: BGS 614
Locus name: Zeocriton 2
Locus symbol: Zeo2

Previous nomenclature and gene symbolization:

Zeocriton with no gene symbol (3, 6).
Zeocriton 2 = Zeo2 (5).
Semidwarf mutant = Mo1 (11).
Rachis internode length QTL on 2HL = *qSIL.ak-2H* (7).

Inheritance:

Monofactorial dominant (1, 7).
Located in chromosome 2HL (1, 7, 12); in 2H bin 13 (1); near SRS marker ABG613 (7); near the cleistogamy 1 (*cly1*) locus (7, 9); *Zeo2.c* is associated with SNP markers 1_0404 to 1_0072 (positions 186.61 to 239.78 cM) in 2HL bins 12 to 14 of the Bowman backcross-derived line BW939; the dense spike traits in the *dsp1.a* stock (likely *Zeo2.c*) is associated with SNP markers 1_0376 to 2_0561 (positions 209.87 to 247.86 cM) in 2HL bins 13 to 14 of the Bowman backcross-derived line BW277; *Zeo2.av* (formerly named *dsp.av*), a *Zeo2* allele with *Pyr1.i* gene, and *Zeo2.d* are associated with SNP markers 2_1315 to 1_0315 (positions 193.08 to 224.35 cM) in 2HL bins 12 to 14 of three Bowman backcross-derived lines from Finish cultivars (BW269, BW661, and BW933), respectively; *Zeo2.h* (previously named *Zeo3.h*) is associated with SNP markers 2_1125 to 2_0293 (positions 206.17 to 234.63 cM) in 2HL bins 13 to 14 of the Bowman backcross-derived line BW940; *Zeo2.j* is associated with SNP markers 2_1370 to 1_1023 (positions 199.54 to 224.35 cM) in 2HL bins 12 to 14 of the Bowman backcross-derived line BW936; a *Zeo2* mutant (with the *eog1.e* gene) is associated with SNP markers 1_1480 to 2_0895 (positions 173.50 to 209.91 cM) in 2HL bins 11 to 13 of the Bowman backcross derived line BW302; *Zeo2.ax* (previously named *dsp.ax*) is associated with SNP markers 2_0064 to 2_0175 (positions 179.99 to 213.08 cM) in 2H bins 11 to 13 of the Bowman backcross-derived line BW270; *Zeo2.ax* in the *ant22.1508* stock is associated with SNP markers 1_1346 to 2_0895 (positions about 165 to 209.87 cM) in 2H bins 11 to 13 of the Bowman backcross-derived line BW022 (2), in 2H bin 13. The *Zeo2* locus is very close to the *Zeo1* locus (2).

Description:

The spikes are compact and remain strap-shaped because all rachis internodes are about the same length. Plants are slightly shorter and spikes contain 2 to 4 more fertile spikelets than those of normal sibs (1). Hayes and Harlan (6) named this phenotype zeocriton (little barley), but they reported that three genes controlled this trait in their cross to zeocriton (8). Plants of the Bowman backcross-derived lines with *Zeo2* alleles in the *Zeo2.c* and *Zeo2.ax* group have small anthers (2/3 of normal length) (4) and are associated with small lodicules (closed flowering or cleistogamy) (7, 9). The rachis internode length of plants in Bowman backcross lines for *Zeo2* alleles averaged 3.3 mm compared to 4.5 mm for Bowman. In some test environments, the BW lines for *Zeo2* genes had 1 to 2 more kernels per spike than Bowman and kernel weights were slightly lower. No effects of the *Zeo2* gene on plant height and grain yield were observed (4).

Origin of mutant:

A naturally occurring variant in two- and six-rowed barley cultivars (5, 7, 10).

Mutational events:

Based on SNP haplotypes similarity for the retained markers in 2HL, the potential *Zeo2* alleles can be placed in three groups (2, 4). *Zeo2.c* was isolated from line 36Ab51

(GSHO 637), which was called “good zeocriton” (4, 10), can be grouped with *Zeo2.ax* from Clho 6880 and Haruna Nijo; *Zeo2.d* and *Zeo2.av* from Aapo and other Finnish cultivars; *Zeo2.h* and *Zeo2.j* from North American six-rowed cultivars Morex (Clho 15773) and Glenn (Clho 15769), respectively (2, 4); a *Zeo2* allele from Golden Melon (OUJ808, PI 263410) in Kanto Nakato Gold (OUJ 518) (7).

Mutant used for description and seed stocks:

Zeo2.c in 36Ab51 (GSHO 637); *Zeo2.c* in Bowman (PI 483237)*4 (GSHO 3433), in Bowman*4 (BW939, NGB 22368); *Zeo2.d* from P11 (Clho 15836) in Bowman*7 (BW933, NGB 22362); *Zeo2.d* from Aapo (PI 467771) via Pokko (PI 467770) in Bowman*4 (BW269, NGB 22094) and *Zeo2.d* with *Pyr1.a* from Aapo (PI 467771) via Pokko (PI 467770) in Bowman*7 (BW661, NGB 22226); *Zeo2.h* from Morex (Clho 15773) mutant (Mo1, Wa11094-81, GSHO 1611) in Bowman*8 (BW940, NGB 22369); *Zeo2.j* from Glenn (Clho 15769) mutant SA121-4-5 in Bowman*7 (BW936, NGB 22365); *Zeo2.ax* from Clho 6880 (Ahang/Twisted Flag/Triple-awn Lemma) in Bowman*5 (BW270, NGB 22095); *Zeo2.ax* with *ant22.1508* from Haruna Nijo (NGB 13705, GSHO 1635) in Bowman*6 (BW022, NGB 20430).

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Prepared:

J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:115.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:193-194.

BGS 621, Calcaroides-c, *Cal-c*

Stock number: BGS 621
Locus name: Calcaroides-c
Locus symbol: *Cal-c*

Previous nomenclature and gene symbolization:
None.

Inheritance:

Monofactorial dominant (5, 6).

Located in chromosome 5HL (7); very close or allelic to *cal-b* (calcaroides-b) locus and near molecular marker WG530 in 5H bin 06 (7); *Cal-c.15* is associated with SNP markers 1_1198 to 1_0869 (positions 73.70 to 264.33 cM) in 5H bins 04 to 13 of the Bowman backcrossed-derived line BW105 (2), in 5H bin 06.

Description:

At the tip of the lemma proper, in a position corresponding to the transition between lemma and awn, the *Cal-c* mutant bear a well-organized ectopic structure, the sac plus pronounced lemma wings (1, 7). The distal awn is short and develops small wings (7). In contrast to the *Kap1* (hooded lemma 1) phenotype, the sac does not develop into an epiphyllous flower. Leaf knots were observed, but leaf curling was not (7). The awn malformation of *Cal-c* mutants is caused by developmental activation of the phytomeric triad separating the lemma from awn (4). Expression of the *Cal-c* phenotype is stronger in homozygotes and more pronounced in spikelets near the tip of the spike (3). In the Bowman backcrossed-derived line BW105, plants were slightly shorter than Bowman and the awns as measured from the tip of the spike were short, 5 vs. 12 cm. Leaf blade widths were about 2/3 of normal length and the spikes had 3 to 4 fewer kernels. Kernels of BW105 were thinner than those of Bowman and weighed about 20% less. Grain yields approached 1/2 of normal (3).

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763) (5, 6).

Mutational events:

Cal-c.15 in Bonus (NGB 114294, GSHO 1567) (6).

Mutant used for description and seed stocks:

Cal-c.15 in Bonus (GSHO 1567, NGB 114294); *Cal-c.15* in Bowman (PI 483237)*4 (GSHO 2188), in Bowman*6 (BW105, NGB 20511).

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Prepared:

U. Lundqvist and J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:122.

Revised:

J.D. Franckowiak and U. Lundqvist. 2011. Barley Genet. Newsl. 41:195-196.

BGS 630, Breviaristatum-s, *Ari-s*

Stock number: BGS 630
Locus name: Breviaristatum-s
Locus symbol: *Ari-s*

Previous nomenclature and gene symbolization:

Breviaristatum-265 = *ari-265* (3).

Inheritance:

Monofactorial incomplete dominant (2).

Located in chromosomes 5H or 7H (1); *Ari-s.265* is associated with SNP markers 2_1177 (position 203.85 cM) in 5H bin 11 and with SNP marker 1_1291 (position 107.44 cM) in 7H bin 07 of the Bowman backcross-derived line BW057 (1). Note that the expression of marker 1_1291 was variable among BW lines.

Description:

Awns of plants homozygous for the *Ari-s.265* allele are about 1/3 normal length and slightly wider than those of normal sibs. The grain is wide and short and has a globose shape. Sterile lateral spikelets and glumes are about half normal length. Rachis internodes are shortened slightly, plants are 3/4 to 5/6 of normal height, and plant vigor is reduced (2). Awns of plants heterozygous for the *Ari-s.265* allele were 3/4 normal length. A slight shortening of other parts of the spike was observed in heterozygotes (2). Compared to Bowman, plants of the Bowman backcross-derived line for *Ari-s.265*, BW057, were 10 to 15% shorter, their awns were about half as long, and rachis internodes were shorter, 3.7 vs. 4.5 mm. Kernel were short, 6.3 vs. 9.7 mm and about 40% lighter, 3.5 vs. 5.8 mg. Grain yields of BW057 were about 1/3 those of Bowman (2).

Origin of mutant:

A gamma-ray induced mutant in Kristina (NGB 1500) (3, 4).

Mutational events:

Ari-s.265 (NGB 116074) in Kristina (4).

Mutant used for description and seed stocks:

Ari-s.265 in Kristina (NGB 116074); *Ari-s.265* in Bowman (PI 483237)*6 (GSHO 3426), in Bowman*7 (BW057, NGB 20405).

References:

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Prepared:

U. Lundqvist and J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:131.
J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:197.

BGS 635, Necroticans 7 *nec7*

Stock number: BGS 635
Locus name: Necroticans 7
Locus symbol: *nec7*

Previous nomenclature and gene symbolization:

Necroticans 45 = *nec-45* (3, 4).

Inheritance:

Monofactorial recessive (4).

Located in chromosomes 1H or 6H or 7H (1); *nec7.45* is associated with SNP markers 1_0186 to 2_0990 (positions 37.21 to 115.07 cM) in 1H bins 04 to 10, with SNP markers 1_0799 to 1_1029 (positions 50.33 to 70.15 cM) in 6H bins 04 to 05, and with SNP markers 1_0971 to 2_0245 (positions 0.00 to 13.19 cM) in 7H bin 01 of the Bowman backcross-derived line BW634 (1), likely in 1H.

Description:

As each tiller of plants homozygous for the *nec7* gene starts to head, dark brown blotches become visible on the leaf blades and sheaths. The blotches are variable in size and irregular in shape. They gradually enlarge and partially coalesce. Blotches range in size from small spots to large ones that may include 1/5 of the leaf blade or more. Some blotches are partially surrounded by a golden or yellowish halo before that region of the leaf dies (2, 4). When *nec7* plants are grown in greenhouses, formation of the dark brown blotches is associated with a distinct musty odor, which persists even after plants ripen (2). Plants of the Bowman backcross-derived line for *nec7.45*, BW634, were about 15% shorter than Bowman plants. The number of kernels per spike for BW634 varied from 2 to 3 more to 2 less. Kernel weights varied from equal to 20% less and grain yields were about 3/4 those of Bowman. The number and size of blotches varies widely across environments (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Kristina (NGB 1500) (4).

Mutational events:

nec7.45 (*nec-45*, NGB 115306, GSHO 2420) in Kristina (4).

Mutant used for description and seed stocks:

nec7.45 in Kristina (GSHO 2420, NGB 115306); *nec7.45* in Bowman (PI 483237)*2, in Bowman*4 (BW634, NGB 22200).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
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4. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J. D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:136.

Revised:

U. Lundqvist and J. D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:198.

BGS 673, Corn stalk 1, *cst1*

Stock number: BGS 673
Locus name: Corn stalk 1
Locus symbol: *cst1*

Previous nomenclature and gene symbolization:

Corn stalk = cs (2).

Inheritance:

Monofactorial recessive (2, 4).

Location in chromosome 5HL (1); Location in chromosome 5HL (1, 2); associated with the T2-7b and T6-7c translocation breakpoints (2); *cst1.a* is associated with SNP markers 2_0653 to 2_1452 (positions 199.0 to 244.39 cM) in 5HL bins 11 to 13 of the Bowman backcross-derived line BW197 (1).

Description:

The *cst1.a* mutant produces a semidwarf unicum plants with thick culms in six rowed barley, which have moderate to very low seed set (4). As *cst1.a* gene was backcrossed into two-rowed barley Bowman, an increase in tillering and improved seed set were observed. Plants of the Bowman backcross-derived line BW197 were about 3/4 normal height and had very compact spikes, 2.8 vs. 4.5 mm. Awns, peduncles, and leaf blades of BW197 were about 3/4 the length of those of Bowman. Kernels of BW197 were slightly shorter than those of Bowman and the average seed weight was 4.5 vs. 5.7 mg. Grain yields of BW197 were very low (3).

Origin of mutant:

An X-ray induced mutant in Husky (Clho 9537) (2).

Mutational events:

cst1.a in Husky (2).

Mutant used for description and seed stocks:

cst1.a in LACZ95469, a six-rowed genetic stock from Lacombe, Alberta (4); *cst1.a* from LACZ95469 in Bowman (PI 483237)*5 (BW197, NGB 22029).

References:

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Prepared:

J.D. Franckowiak 2011. *Barley Genet. Newsl.* 41:199.

BGS 678, Breviaristatum-u, *ari-u*

Stock number: BGS 678
Locus name: Breviaristatum-u
Locus symbol: *ari-u*

Previous nomenclature and gene symbolization:

Breviaristatum-245 = *ari.245* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 2HS (1); *ari-u.245* is associated with SNP markers 2_0609 to 2_1377 (positions about 13.0 to 20.11 cM) from Foma in 2H bin 02 of the Bowman backcrossed-derived line BW031 (1), in 2H bin 02.

Description:

Plants have reduced awn length, about 2/3 of normal with an undulated awn tip and an erect or brachytic growth habit (3). In the Bowman backcross-derived line for *ari-u.245*, BW031, a brachytic-like growth habit was observed, but expression of morphological traits was variable among nurseries with plant growth more reduced in moisture stressed nurseries. BW031 plants were 10 to 40% shorter and peduncles were 20 to 40% shorter compared to Bowman plants. Awn lengths of BW031 were 2/3 to 3/4 those for Bowman and rachis internode length varied from 2.9 to 4.3 mm compared to about 4.5 mm for Bowman. Kernels of BW031 were slightly smaller and 20% lighter. Grain yields varied from less than 1/3 to 3/4 of the Bowman yields (2). The variability in trait expression over environments observed in BW031 could be described as phenotypic plasticity, see Lacaze et al. (4).

Origin of mutant:

An N-methyl-N-nitrosourea induced mutant in Foma (Clho 11333) (3, 5).

Mutational events:

ari-u.245 (NGB 116054) in Foma (2, 3).

Mutant used for description and seed stocks:

ari-u.245 (NGB 116054) in Foma; *ari-u.245* via ND14701 in Bowman (PI 483237)*5 (BW031, NGB 20439).

References:

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Prepared:

J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:200.

BGS 679, Accordion rachis 4, *acr4*

Stock number: BGS 679
Locus name: Accordion rachis 4
Locus symbol: *acr4*

Previous nomenclature and gene symbolization:

Accordion rachis 3 = *acr-3* (3).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 2H or/and 6HL (1); *acr4.3* is associated with SNP markers 1_0891 to 2_1533 (positions 54.47 to 141.56 cM) in 2H bins 05 to 10 of the Bowman backcrossed-derived line BW004 and associated with SNP markers 1_0015 to 2_0733 (positions 160.38 to 180.69 cM) in 6HL bins 10 to 11 of BW004 (1).

Description:

The *acr4.3* mutant plants have multiple changes from normal besides elongated rachis internodes (3). Plant height is reduced, maturity is delayed, awns are short, the basal rachis internode is elongated, and partial fertility occurs (3). Plants of the Bowman backcross-derived line for *acr4.3*, BW004, showed similar alterations in plant morphology. The two largest DNA segments of BW004 in which donor parent SNP markers are retained overlap regions where lax spike loci have been mapped: 2HL (*acr1*, accordion rachis 1) and 6HL (*lax-c*, *laxatum-c*) (1, 2).

Origin of mutant:

An ethylene imine induced mutant in Bonus (PI 189763) (3).

Mutational events:

acr4.3 (NGB 115043) in Bonus (3).

Mutant used for description and seed stocks:

acr4.3 (NGB 115043) Bonus; *acr4.3* in Bowman (PI 483237)*3 (BW004, NGB 20412).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
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Prepared:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:201.

BGS 680, Breviaristatum-v, *ari-v*

Stock number: BGS 680
Locus name: Breviaristatum-v
Locus symbol: *ari-v*

Previous nomenclature and gene symbolization:

Breviaristatum-137 = *ari.137* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 5HS (1); *ari-v.137* is associated with SNP markers 2_1065 to 2_0265 (positions about 40.91 to 94.02 cM) in 5H bins 02 to 04 of Bowman backcrossed-derived line BW026 (1).

Description:

The mutant was selected as having slight shorter awns with weak calcaroides expression compared to the parental line Foma and a slight increase in plant height (3). The Bowman backcross-derived line for *ari-v.137*, BW026, was about 15% taller than Bowman, approximately 99 vs. 87 cm (2). The awns were 1 to 3 cm shorter than those of Bowman. Kernels of BW026 were 15% longer than those of Bowman and weighed 5 to 10% more. Grain yields of BW026 were similar to those of Bowman, but their test weights were slightly lower (2).

Origin of mutant:

An N-methyl-N-nitrosourea induced mutant in Foma (Clho 11333) (3, 4).

Mutational events:

ari-v.137 (NGB 115947) in Foma (3, 4).

Mutant used for description and seed stocks:

ari-v.137 (NGB 115947) in Foma; *ari-v.137* via ND15006 in Bowman (PI 483237)*5 (BW026, NGB 20434).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
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Prepared:

J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:202.